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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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10/728,509

12/05/2003

Hong Zhang

ISPH-0803

9823

55389 7590 01/03/2008
KNOBBE, MARTENS, OLSON & BEAR, LLP
2040 MAIN STREET
FOURTEENTH FLOOR
IRVINE, CA 92614

EXAMINER

ZARA, JANE J

ART UNIT

PAPER NUMBER

1635

MAIL DATE

DELIVERY MODE

01/03/2008

PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary

Application No.

10/728,509

Applicant(s)

ZHANG ET AL.

Examiner

Jane Zara

Art Unit

1635

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 16 November 2007.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-9 and 11-18 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-9 and 11-18 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application
- 6) ☒ Other: Sequence Alignment Data

DETAILED ACTION

This Office action is in response to the communication filed 11-16-07.

Claims 1-9, 11-18 are pending in the instant application.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Election/Restrictions

SEQ ID Nos. other than SEQ ID No. 64 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on 11-16-07.

Applicant's election without traverse of SEQ ID No. 64 in the reply filed on 11-16-07 is acknowledged.

Response to Arguments and Amendments

Withdrawn Rejections

Any rejections not repeated in this Office action are hereby withdrawn.

Rejections Necessitated by Amendments

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-9, 11-18 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In claim 1, line 2, it is unclear whether the recited phrase "12 linked nucleosides" refers to contiguously linked nucleobases, or non-contiguous nucleobases. Appropriate clarification is required.

Claims 15 and 16 recite compounds comprising or consisting of "any of" a single sequence. The metes and bounds of the claimed invention cannot be determined. Appropriate correction is required.

It is unclear whether the description of "each internucleoside linkage is a phosphorothioate linkage" (last line of claim 18) refers to the entire oligonucleotide, or the gap or wing segments only. Appropriate clarification is required.

Claim Rejections - 35 USC § 102/103

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all

obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 1-3, 7, 11, and 13-15 are rejected under 35 U.S.C. 102(e) as being anticipated by or, in the alternative, under 35 U.S.C. 103(a) as obvious over Mittman et al (USPN 6,821,724).

Mittman et al (USPN 6,821,724) teach compositions and methods of inhibiting a known target gene of interest comprising administering an antisense oligonucleotide between 12-30 nucleobases in length comprising at least 12 linked nucleosides of SEQ ID No. 64, a pharmaceutically acceptable diluent, and which oligonucleotide optionally further comprises modified nucleobases and internucleotide linkages(see SEQ ID No. 2494 of Mittman et al, see also col. 1-2 and 4, claim 1; see also the accompanying sequence alignment data). The burden of establishing whether the prior art oligonucleotide has the function of inhibiting gene expression as claimed falls to applicant. See (In re Best, 562 F.2d 1252, 1255, 195 USPQ 430, 433-434 (CCPA 1977): "Where, as here, the claimed and prior art products are identical or substantially identical, or are produced by identical or substantially identical processes, the PTO can require an applicant to prove that the prior art products do not necessarily or inherently possess the characteristics of his claimed product... Whether the rejection is based on 'inherency' under 35 USC 102, on 'prima facie obviousness' under 35 USC 103, jointly or alternatively, the burden of proof is the same, and its fairness is evidenced b the PTO's inability to manufacture products or to obtain and compare prior art products

[footnote omitted]." See also MPEP 2112: "[T]he PTO can require an applicant to prove that the prior art products do not necessarily or inherently possess the characteristics of his [her] claimed product." The MPEP at 2112 citing In re Fitzgerald 205 USPQ 594, 596 (CCPA 1980), quoting In re Best 195 USPQ 430 as per above. Therefore, absent evidence to the contrary, since the oligonucleotides disclosed by Zhou et al meet all of the structural limitations of the instantly claimed invention, it would necessarily be presumed to have the functionality claimed, of specifically inhibiting expression of BCL2-associated x protein in vitro.

Therefore, absent evidence to the contrary, claims 1, 2, 10, 11, and 13 are anticipated by or, in the alternative, obvious over Mittman et al.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 1-9, 11-18 are rejected under 35 U.S.C. 103(a) as being unpatentable over Mittman et al (USPN 6,821,724) as applied to claims 1-3, 7, 11, and 13-15 above, in view of Korsmeyer (USPN 6,500,626) and further in view of Milner et al and McKay insofar as the claims are drawn to compositions and methods of inhibiting the expression of the BCL2-associated x protein in vitro comprising administration of a

composition comprising an antisense oligonucleotide between 12-30 nucleobases in length comprising at least 12 linked nucleosides of nucleobases of SEQ ID NO: 64, which oligonucleotide comprises a phosphorothioate internucleotide linkage, a 2'-O-methoxyethyl sugar moiety and a 5'-methyl-cytosine, and which is optionally a chimeric oligonucleotide, and which composition further comprises a colloidal dispersion system and gap segment consisting of ten linked deoxynucleotides, a 5' wing segment consisting of five linked nucleotides, a 3' wing segment consisting of five linked nucleotides, and which gap segment is between the 5' and 3' wings, and each wing comprises a 2'-O-methoxyethyl sugar and wherein each internucleoside linkage is a phosphorothioate linkage.

Mittman et al (USPN 6,821,724) is relied upon as cited in the 102/103 rejection above.

Mittman does not teach antisense oligonucleotides comprising phosphorothioate internucleotide linkages, 2'-O-methoxyethyl modified sugar moieties or 5-methyl cytosine nucleobases, nor chimeric antisense oligonucleotides, nor colloidal dispersion systems, gapmers.

Korsmeyer (6,500,626) teach the inhibition of expression of SEQ ID No. 17, encoding the BCL2-associated x protein, using antisense oligonucleotides (see col. 29 and col. 46, lines 54-56).

Milner et al (Nature Biotech. 15: 537-541, 1997) teach methods of designing and testing antisense oligonucleotides for their ability to specifically hybridize and inhibit the expression of a target nucleic acid of known nucleotide sequence in vitro, including in

the 5', 3' and stop codon regions of the target gene (See figure 1 on p 538 and figures 5-7 on pages 539-540).

McKay et al (USPN 6,133,246, 10-17-00) teach colloidal dispersion compositions comprising antisense oligonucleotides between 12 and 30 nucleobases in length which optionally comprise modified internucleotide linkages including phosphorothioate linkages, modified nucleobases including 5-methylcytosine, modified sugar moieties including 2'-O-methoxyethyl sugars, and wherein the antisense is optionally a chimeric oligonucleotide, and antisense oligonucleotides optionally design choices of modifications comprising 5' wing segments consisting of five linked nucleotides, 3' wing segments consisting of five linked nucleotides, and a gap segment between the 5' and 3' wings, wherein each wing comprises a 2'-O-methoxyethyl sugar and wherein each internucleoside linkage is a phosphorothioate linkage, and which antisense targets various regions of a target gene. McKay et al also teach the in vitro inhibition and screening of modulators (e.g. of various antisense oligonucleotides between 12-30 nucleobases that specifically hybridize with the target gene).

It would have been obvious to one of ordinary skill in the art to design and utilize antisense oligonucleotides between 12-20 nucleobases in length comprising at least 12 contiguous nucleobases of SEQ ID NO. 64 to inhibit the expression of SEQ ID No. 17, encoding the BCL2-associated x protein (BAX) in vitro, because Mittman teaches this antisense sequence, and Milner et al and McKay teach the ability to design and assess antisense oligonucleotides for their ability to inhibit the expression of a target gene of known nucleotide sequence in vitro, including various regions of the target gene of

interest, using routine screening assays that are well known in the art (see Milner at pages 539-540 and McKay at col. 6-15). It would have been obvious to one of ordinary skill in the art to target and inhibit the expression of BCL2-associated x protein in vitro comprising the administration of antisense oligonucleotides between 12-30 nucleobases because Mittman teaches such antisense sequences for targeting and inhibiting the expression of a known target gene, Milner teaches methods of designing and assessing antisense oligonucleotides between 8-50 nucleobases for their ability to target and inhibit the expression of a known target gene in vitro. One of ordinary skill in the art would have been motivated to utilize such a method of finding optimal antisense oligonucleotides between 12-30 nucleobases which best target and inhibit BCL2-associated x protein expression in order to study this target molecule's role in apoptosis, and its role in pathologies related to aberrant expression of BAX, including such conditions as Parkinson's, Alzheimer's.

One of ordinary skill in the art would have expected that the methods of designing and assessing antisense oligonucleotides for inhibiting a target gene of known sequence, which were taught by Milner et al, and also taught by McKay to be routine for a previously characterized target gene, would successfully be used to identify numerous antisense oligonucleotides (between 12-30 nucleobases) for the in vitro inhibition of BCL2-associated x protein expression. One of ordinary skill in the art would have been motivated to incorporate the nucleobase, internucleotide linkage and sugar modifications, as well as chimeric structures, into antisense oligonucleotides because such modifications (including 5-methyl cytosine, 2'-O-methoxyethyl and

phosphorothioate linkages) have been taught previously by McKay et al to increase target binding, cellular uptake and antisense stability. One of ordinary skill in the art would have expected that the delivery of modified antisense oligonucleotides to target cells harboring BCL2-associated x protein, which antisense specifically hybridize with the target nucleic acid encoding BCL2-associated x protein (e.g. of the 3' UTR of SEQ ID No. 17), would lead to inhibition of expression of BCL2-associated x protein in vitro.

Therefore, the invention as a whole would have obvious to one of ordinary skill in the art at the time the invention was made.

Conclusion

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire **THREE MONTHS** from the mailing date of this action. In the event a first reply is filed within **TWO MONTHS** of the mailing date of this final action and the advisory action is not mailed until after the end of the **THREE-MONTH** shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than **SIX MONTHS** from the mailing date of this final action.

Certain papers related to this application may be submitted to Art Unit 1635 by facsimile transmission. The faxing of such papers must conform with the notices

Application/Control Number:
10/728,509
Art Unit: 1635

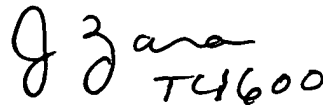
Page 10

published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 C.F.R. ' 1.6(d)). The official fax telephone number for the Group is 571-273-8300. NOTE: If Applicant does submit a paper by fax, the original signed copy should be retained by applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jane Zara whose telephone number is (571) 272-0765. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James Douglas Schultz, can be reached on (571) 272-0763. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Jane Zara
12-26-07

Handwritten signature of Jane Zara in cursive, with the number 74600 written below it.

JANE ZARA, PH.D.
PRIMARY EXAMINER

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244597

ACCESS DB #

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Scientific and Technical Information Center

SEARCH REQUEST FORM

CRFE

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 11-30-07
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 101728,509
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: AS MODN of BCL-2 Assoc.
Inventors (please provide full names): H. Zhang et al

Earliest Priority Date: 12-8-03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No 64
① - oligo search - limit to 50 NTS.
② { Score over length 70 - 100% IDents.
size range 12 - 30 Nucleotides.

please include Antisense Searches

Thanks

64-20na
LB

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Type of Search

Vendors and cost where applicable

Searcher: _____

____ NA Sequence (#)

____ STN

____ Dialog

Searcher Phone #: _____

____ AA Sequence (#)

____ Questel/Orbit

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Searcher Location: _____

____ Structure (#)

____ Westlaw

____ WWW/Internet

Date Searcher Picked Up: _____

____ Bibliographic

____ In-house sequence systems

Date Completed: _____

____ Litigation

____ Commercial
____ Interference

____ Oligomer
____ SPDI

____ Score/Length
____ Encode/Transl

Searcher Prep & Review Time: _____

____ Fulltext

____ Other (specify)

Online Time: _____

____ Other


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; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
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; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
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; SOFTWARE: PatentIn version 3.3
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; TYPE: RNA
; ORGANISM: Human
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; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
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Sequence
Alignment
DATA

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; Sequence 2494, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2494
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; TYPE: DNA
; ORGANISM: Mus musculus
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US-10-719-900-62297/c
; Sequence 62297, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 62297
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; ORGANISM: Mus musculus
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:12:43 ; Search time 935 Seconds

(without alignments)
80.129 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

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Scoring table:

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Gapop 60.0 , Gapext 60.0

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Word size : 1

Total number of hits satisfying chosen parameters: 6387464

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 11: /EMC_Celerra_SID22/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	14	70.0	37	US-09-060-299-146	Sequence 146, App
2	14	70.0	37	US-09-402-923A-146	Sequence 146, App
3	14	70.0	37	US-10-331-907-146	Sequence 146, App
C 4	13	65.0	20	US-10-310-914B-157899	Sequence 157899,
5	13	65.0	20	US-10-310-914B-1165052	Sequence 1165052,
C 6	13	65.0	23	US-10-310-914B-1175079	Sequence 1175079,
C 7	13	65.0	25	US-09-396-196G-2494	Sequence 2494, App
C 8	13	65.0	25	US-10-719-900-62297	Sequence 62297, A
9	13	65.0	25	US-10-719-900-76493	Sequence 76493, A
C 10	13	65.0	25	US-10-719-900-168653	Sequence 168653,
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C 12	13	65.0	25	US-10-719-900-974745	Sequence 974745,
C 13	13	65.0	25	US-10-719-900-975477	Sequence 975477,
C 14	13	65.0	50	US-10-131-827-5954	Sequence 5954, App
C 15	13	65.0	50	US-10-131-827-6319	Sequence 6319, App
C 16	13	65.0	50	US-10-131-831-5954	Sequence 5954, App
C 17	13	65.0	50	US-10-131-831-6319	Sequence 6319, App
C 18	13	65.0	50	US-10-325-899-5954	Sequence 5954, App
C 19	13	65.0	50	US-10-325-899-5954	Sequence 5954, App
C 20	12	60.0	15	US-08-584-040-8471	Sequence 8471, App
C 21	12	60.0	15	US-09-371-772B-4126	Sequence 4126, App
C 22	12	60.0	15	US-09-685-664B-4126	Sequence 4126, App

C 23	12	60.0	15	US-10-138-674B-4126	Sequence 4126, Ap
C 24	12	60.0	17	US-08-584-040-3879	Sequence 3879, Ap
C 25	12	60.0	17	US-08-584-040-3880	Sequence 3880, Ap
C 26	12	60.0	17	US-09-371-772B-1646	Sequence 1646, Ap
C 27	12	60.0	17	US-09-371-772B-1647	Sequence 1647, Ap
C 28	12	60.0	17	US-09-371-772B-6253	Sequence 6253, Ap
C 29	12	60.0	17	US-09-371-772B-6254	Sequence 6254, Ap
C 30	12	60.0	17	US-09-685-664B-1646	Sequence 1646, Ap
C 31	12	60.0	17	US-09-685-664B-1647	Sequence 1647, Ap
C 32	12	60.0	17	US-10-138-674B-1646	Sequence 1646, Ap
C 33	12	60.0	17	US-10-138-674B-1647	Sequence 1647, Ap
C 34	12	60.0	17	US-10-138-674B-6253	Sequence 6253, Ap
C 35	12	60.0	17	US-10-138-674B-6254	Sequence 6254, Ap
C 36	12	60.0	17	US-10-138-674B-8571	Sequence 8571, Ap
C 37	12	60.0	19	US-10-310-914B-1191074	Sequence 1191074,
38	12	60.0	25	US-08-997-685A-30	Sequence 30, Appl
39	12	60.0	25	US-09-086-436-18	Sequence 18, Appl
C 40	12	60.0	25	US-10-719-900-113603	Sequence 113603,
C 41	12	60.0	25	US-10-719-900-464231	Sequence 464231,
C 42	12	60.0	25	US-10-719-900-582537	Sequence 582537,
C 43	12	60.0	25	US-10-719-900-632716	Sequence 632716,
C 44	12	60.0	25	US-10-719-900-657676	Sequence 657676,
45	12	60.0	25	US-10-719-900-731099	Sequence 731099,

ALIGNMENTS

RESULT 1

US-09-060-299-146
; Sequence 146, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,299
; FILING DATE: 15-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-060-299-146

Query Match

Best Local Similarity 70.0%; Score 14; DB 3; Length 37;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
|||||
DB 14 CCAGTTGAAGTTGC 27

RESULT 2

US-09-402-923A-146

Sequence 146, Application US/09402923A

Patent No. 6555654

GENERAL INFORMATION:

APPLICANT: Todd, John A

Hess, John W

Caskey, Charles T

Cox, Roger D

Gerhold, David

Hammond, Holly

Hey, Patricia

Kawaguchi, Yoshihiko

Merriman, Tony R

Metzker, Michael L

TITLE OF INVENTION: No. 6555654e1 LDL-Receptor

NUMBER OF SEQUENCES: 455

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye

STREET: 1100 No. 6555654th Glebe Road, Eighth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: US

ZIP: VA 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,923A

FILING DATE: 14-Feb-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01102

FILING DATE: 15-APR-1998

APPLICATION NUMBER: US 60/043,553

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 60/048,740

FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: B.J.Sadoff

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 620-81

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4091

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 146:

US-09-402-923A-146

Query Match

Best Local Similarity 70.0%; Score 14; DB 3; Length 37;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
|||||
DB 14 CCAGTTGAAGTTGC 27

RESULT 3

US-10-331-907-146

Sequence 146, Application US/10331907

Patent No. 7244577

GENERAL INFORMATION:

APPLICANT: Todd, John A

Hess, John W

Caskey, Charles T

Cox, Roger D

Gerhold, David

Hammond, Holly

Hey, Patricia

Kawaguchi, Yoshihiko

Merriman, Tony R

Metzker, Michael L

TITLE OF INVENTION: No. 7244577e1 LDL-Receptor

NUMBER OF SEQUENCES: 455

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye

STREET: 1100 No. 7244577th Glebe Road, Eighth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: US

ZIP: VA 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/331,907

FILING DATE: 31-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,923A

FILING DATE: 14-Feb-2001

APPLICATION NUMBER: PCT/GB98/01102

FILING DATE: 15-APR-1998

APPLICATION NUMBER: US 60/043,553

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 60/048,740

FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: B.J.Sadoff

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 620-81

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4091

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 146:

US-10-331-907-146

Query Match

Best Local Similarity 70.0%; Score 14; DB 5; Length 37;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
|||||
DB 14 CCAGTTGAAGTTGC 27

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RESULT 4
US-10-310-914B-157899/c
; Sequence 157899, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157899
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-157899

Query Match      65.0%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
      |||||
Db      14 AGTTGAAGTTGCC 2

RESULT 5
US-10-310-914B-1165052
; Sequence 1165052, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1165052
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1165052

Query Match      65.0%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
      |||||
Db      14 AGTTGAAGTTGCC 2

RESULT 6
US-10-310-914B-1175079/c
; Sequence 1175079, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1175079
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1175079

Query Match      65.0%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGAAG 13
      |||||
Db      21 GCCCCAGTTGAAG 9

RESULT 7
US-09-396-196G-2494/c
; Sequence 2494, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2494
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-2494

Query Match      65.0%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTGCCG 19
      |||||
Db      17 GTTGAAGTTGCCG 5

RESULT 8
US-10-719-900-62297/c
; Sequence 62297, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 62297
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-62297

Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
```

```
; SEQ ID NO 1175079
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1175079

Query Match      65.0%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGAAG 13
      |||||
Db      21 GCCCCAGTTGAAG 9

RESULT 7
US-09-396-196G-2494/c
; Sequence 2494, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2494
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-2494

Query Match      65.0%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTGCCG 19
      |||||
Db      17 GTTGAAGTTGCCG 5

RESULT 8
US-10-719-900-62297/c
; Sequence 62297, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 62297
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-62297

Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
```

```
Db      16 AGTTGAAGTTGCC 4
RESULT 9
US-10-719-900-76493
; Sequence 76493, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 76493
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-76493
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 CCCAGTTGAAGT 14
Db      9 CCCAGTTGAAGT 21
RESULT 10
US-10-719-900-168653/c
; Sequence 168653, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 168653
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-168653
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 AGTTGAAGTTGCC 18
Db      18 AGTTGAAGTTGCC 6
RESULT 11
US-10-719-900-311855
; Sequence 311855, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 311855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-311855
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 CCCAGTTGAAGTT 15
Db      8 CCCAGTTGAAGTT 20
RESULT 12
US-10-719-900-974745/c
; Sequence 974745, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 974745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-974745
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 AGTTGAAGTTGCC 18
Db      22 AGTTGAAGTTGCC 10
RESULT 13
US-10-719-900-975477/c
; Sequence 975477, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 975477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-975477
Query Match      65.0%; Score 13; DB 5; Length 25;
```

Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 19
Db 20 GTTGAAGTTGCC 8

RESULT 14

US-10-131-827-5954/c
; Sequence 5954, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5954
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-5954

Query Match 65.0%; Score 13; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18
Db 14 AGTTGAAGTTGCC 2

RESULT 15

US-10-131-827-6319/c
; Sequence 6319, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6319
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6319

Query Match 65.0%; Score 13; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18
Db 14 AGTTGAAGTTGCC 2

Search completed: December 3, 2007, 16:28:20
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OM nucleic - nucleic search, using sw model
Run on: December 3, 2007, 15:56:26 ; Search time 12284 Seconds
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Title: US-10-728-509-64
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Scoring table: OLIGO_NUC
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16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	16	80.0	20	2	DD248708	DD248708 Screening
3	16	80.0	20	2	DD402954	DD402954 Screening
4	16	80.0	20	2	DD404058	DD404058 Method of
5	14	70.0	25	2	CS174774	CS174774 Sequence
6	14	70.0	37	2	BD106103	BD106103 Novel LDL
7	14	70.0	37	2	AR305192	AR305192 Sequence
8	14	70.0	37	2	AR309296	AR309296 Sequence
9	14	70.0	37	2	EA268023	EA268023 Sequence
10	13	65.0	20	2	AX488224	AX488224 Sequence
11	13	65.0	50	2	EA258028	EA258028 Sequence
12	13	65.0	50	2	EA258393	EA258393 Sequence
13	13	65.0	50	2	AR686525	AR686525 Sequence
14	13	65.0	50	2	AR686890	AR686890 Sequence
15	13	65.0	50	2	AR827293	AR827293 Sequence
16	13	65.0	50	2	AR827658	AR827658 Sequence
17	12	60.0	15	2	AR192983	AR192983 Sequence

C 18	12	60.0	15	2	AR326724	AR326724 Sequence
C 19	12	60.0	15	2	AR600184	AR600184 Sequence
C 20	12	60.0	15	2	AR843823	AR843823 Sequence
C 21	12	60.0	17	2	CS508144	CS508144 Sequence
C 22	12	60.0	17	2	DD126995	DD126995 NUCLEIC A
C 23	12	60.0	17	2	AR188391	AR188391 Sequence
C 24	12	60.0	17	2	AR188392	AR188392 Sequence
C 25	12	60.0	17	2	AR324244	AR324244 Sequence
C 26	12	60.0	17	2	AR324245	AR324245 Sequence
C 27	12	60.0	17	2	AR328851	AR328851 Sequence
C 28	12	60.0	17	2	AR328852	AR328852 Sequence
C 29	12	60.0	17	2	AR597704	AR597704 Sequence
C 30	12	60.0	17	2	AR597705	AR597705 Sequence
C 31	12	60.0	17	2	AR841343	AR841343 Sequence
C 32	12	60.0	17	2	AR841344	AR841344 Sequence
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C 34	12	60.0	17	2	AR845951	AR845951 Sequence
C 35	12	60.0	17	2	AR848268	AR848268 Sequence
C 36	12	60.0	19	8	AJ229007	AJ229007 Artificia
C 37	12	60.0	20	2	AX204804	AX204804 Sequence
C 38	12	60.0	21	2	CS498174	CS498174 Sequence
C 39	12	60.0	21	2	DD440518	DD440518 siRNA Med
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C 41	12	60.0	21	2	DD440520	DD440520 siRNA Med
C 42	12	60.0	21	2	DD440521	DD440521 siRNA Med
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ALIGNMENTS

RESULT 1
DD236265
LOCUS DD236265 20 bp DNA linear PAT 26-APR-2006
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor.
ACCESSION DD236265
VERSION DD236265.1 GI:94046395
KEYWORDS WO 2005093082-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakagawara,A. and Ozaki,T.
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor
JOURNAL Patent: WO 2005093082-A 16 06-OCT-2005;
COMMENT Hisamitsu Pharmaceutical Co Inc
OS Artificial
PN WO 2005093082-A/16
PD 06-OCT-2005
PF 23-MAR-2005 WO 2005JP005247
PR 14-JUN-2004 JP 200 4-176107,26-MAR-2004 JP 200 4-093266 PI
akira nakagawara.toshifumi ozaki
CC primer for Bax
FH Key Location/Qualifiers.
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LOCUS DD248708 20 bp DNA linear PAT 18-MAY-2006
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis accelerator and an apoptosis inhibitor.
ACCESSION DD248708
VERSION DD248708.1 GI:99024603
KEYWORDS JP 2005304470-A/16.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakagawara,A. and Ozaki,T.
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis accelerator and an apoptosis inhibitor
JOURNAL Patent: JP 2005304470-A 16 04-NOV-2005;
Hisamitsu Pharmaceutical Co Inc
COMMENT OS Artificial
PN JP 2005304470-A/16
PD 04-NOV-2005
PF 14-JUN-2004 JP 2004176107
PI akira nakagawara,toshifumi ozaki
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FH Key Location/Qualifiers.
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Db 1 CAGTTGAAGTTCGCGT 16

RESULT 3
DD402954
LOCUS DD402954 20 bp DNA linear PAT 21-FEB-2007
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis inhibitor.
ACCESSION DD402954
VERSION DD402954.1 GI:126146805
KEYWORDS JP 2006223265-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakagawara,A. and Ozaki,T.
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis inhibitor
JOURNAL Patent: JP 2006223265-A 8 31-AUG-2006;
Hisamitsu Pharmaceutical Co Inc
COMMENT OS Homo sapiens
PN JP 2006223265-A/8
PD 31-AUG-2006
PF 21-FEB-2005 JP 2005044554
PI akira nakagawara,toshifumi ozaki
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Db 1 CAGTTGAAGTTCGCGT 16

RESULT 4
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LOCUS DD404058 20 bp DNA linear PAT 21-FEB-2007
DEFINITION Method of screening a gene related to a quantity of HCV.
ACCESSION DD404058
VERSION DD404058.1 GI:126149401
KEYWORDS WO 2006085407-A/21.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Baumi,M. and Takayama,T.
TITLE Method of screening a gene related to a quantity of HCV
JOURNAL Patent: WO 2006085407-A 21 17-AUG-2006;
Nihon University
COMMENT OS Artificial
PN WO 2006085407-A/21
PD 17-AUG-2006
PF 30-SEP-2005 WO 2005JP018573
PR 09-FEB-2005 JP 05P 033707
PI mariko esumi,tadatoshi takayama
CC primer
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Db 1 CAGTTGAAGTTCGCGT 16

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DEFINITION Sequence 13 from Patent WO2005090394.
ACCESSION CS174774
VERSION CS174774.1 GI:77625627
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Oswald,S., Weckbecker,C., Huthmacher,K., Gerasimova,T.,
Novikov,A., Ryabchenko,L., Yankenko,A. and Egorova,K.
TITLE Cyanide tolerant nitrilhydratases
JOURNAL Patent: WO 2005090394-A 13 29-SEP-2005;
DEGUSSA AG (DE)
FH Key Location/Qualifiers.
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Db 17 GTTGAAGTTGCCGT 4
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RESULT 6
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LOCUS      Novel LDL-receptor.
DEFINITION Novel LDL-receptor.
ACCESSION BD106103
VERSION   BD106103.1 GI:23200921
KEYWORDS  JP 2002501376-A/118.
SOURCE    Chlamydia sp.
ORGANISM  Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (bases 1 to 37)
AUTHORS  Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H.
and Hey,P.
TITLE     Novel LDL-receptor
JOURNAL   Patent: JP 2002501376-A 118 15-JAN-2002;
          THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
          INC
COMMENT   PN JP 2002501376-A/118
          PD 15-JAN-2002
          PF 15-APR-1998 JP 1998543635
          PR 15-APR-1997 US 60/043553.05-JUN-1997 US 60/048740 PI
          JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES
          THOMAS CASKEY,ROGER
          PI DAVID COX,
          PI DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY
          PC C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,
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QY 4 CCAGTTGAAGTTGC 17
Db 14 CCAGTTGAAGTTGC 27
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RESULT 7
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LOCUS      AR305192
DEFINITION Sequence 146 from patent US 6545137.
ACCESSION  AR305192
VERSION   AR305192.1 GI:31694502
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 37)
AUTHORS  Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
          Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
          Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
          Receptor
          Patent: US 6545137-A 146 08-APR-2003;
          Location/Qualifiers
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Db 14 CCAGTTGAAGTTGC 27
|||||
|

RESULT 8
AR309296
LOCUS      AR309296
DEFINITION Sequence 146 from patent US 6555654.
ACCESSION  AR309296
VERSION   AR309296.1 GI:31701301
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 37)
AUTHORS  Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
          Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
          Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
          LDL-receptor
          Patent: US 6555654-A 146 29-APR-2003;
          The Wellcome Trust Limited as Trustee for the Wellcome Trust;
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Db 14 CCAGTTGAAGTTGC 27
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RESULT 9
EA268023
LOCUS      EA268023
DEFINITION Sequence 146 from patent US 7244577.
ACCESSION  EA268023
VERSION   EA268023.1 GI:155713612
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 37)
AUTHORS  Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
          Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
          Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
          Method of screening for modulator of LRP5 activity
          Patent: US 7244577-A 146 17-JUL-2007;
          Merck & Co., Inc.; Rahway, NJ;
          US;
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Db 14 CCAGTTGAAGTTGCC 27

RESULT 10
AX488224/c
LOCUS AX488224 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 5524 from Patent WO02053728.
ACCESSION AX488224
VERSION AX488224.1 GI:22322304
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Mitosporic Saccharomycetales; Candida.

REFERENCE 1
Roemer T., Jiang B., Boone C., Bussey H. and Ohlsen K.L.
AUTHORS Gene disruption methodologies for drug target discovery
TITLE Patent: WO 02053728-A 5524 11-JUL-2002;
JOURNAL Ellura Pharmaceuticals, Inc. (US)
FEATURES
source 1. .20
Location/Qualifiers
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QY 7 GTTGAAGTTGCCG 19
|||||
Db 17 GTTGAAGTTGCCG 5

RESULT 11
EA258028/c
LOCUS EA258028 50 bp DNA linear PAT 14-AUG-2007
DEFINITION Sequence 5954 from patent US 7235358.
ACCESSION EA258028
VERSION EA258028.1 GI:155699406
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wohlgenuth, J., Fry, K., Woodward, R., Ly, N. and Prentice, J.
TITLE Methods and compositions for diagnosing and monitoring transplant rejection
JOURNAL Patent: US 7235358-A 5954 26-JUN-2007;
Expression Diagnostics, Inc.; South San Francisco, CA;
US;
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source Location/Qualifiers
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Db 14 AGTTGAAGTTGCC 2

RESULT 12
EA258393/c
LOCUS EA258393 50 bp DNA linear PAT 14-AUG-2007
DEFINITION Sequence 6319 from patent US 7235358.
ACCESSION EA258393
VERSION EA258393.1 GI:155699771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wohlgenuth, J., Fry, K., Woodward, R., Ly, N. and Prentice, J.
TITLE Methods and compositions for diagnosing and monitoring transplant rejection
JOURNAL Patent: US 7235358-A 6319 26-JUN-2007;
Expression Diagnostics, Inc.; South San Francisco, CA;
US;
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Db 14 AGTTGAAGTTGCC 2

RESULT 14
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LOCUS AR686890 50 bp DNA linear PAT 12-SEP-2005
DEFINITION Sequence 6319 from patent US 6905827.
ACCESSION AR686890
VERSION AR686890.1 GI:74468660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)

AUTHORS Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.
TITLE Methods and compositions for diagnosing or monitoring auto immune
and chronic inflammatory diseases
JOURNAL Patent: US 6905827-A 6319 14-JUN-2005;
FEATURES Expression Diagnostics, Inc.; So. San Francisco, CA
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Db 14 AGTTGAAGTTGCC 2

RESULT 15
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LOCUS AR827293 50 bp DNA linear PAT 10-AUG-2006
DEFINITION Sequence 5954 from patent US 7026121.
ACCESSION AR827293
VERSION AR827293.1 GI:111851108
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 50)
AUTHORS Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.
TITLE Methods and compositions for diagnosing and monitoring transplant
rejection
JOURNAL Patent: US 7026121-A 5954 11-APR-2006;
Expression Diagnostics, Inc.; South San Francisco, CA;
US;

FEATURES Location/Qualifiers
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Search completed: December 3, 2007, 19:21:28
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GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:46:12 ; Search time 2633 Seconds
(without alignments)
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Title: US-10-728-509-64

Perfect score: 20

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 63

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum Score over Length 70%
Listing first 1000 summaries

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2: gb_pat.*

3: gb_ph.*

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9: gb_un.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
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27	8.8	73.3	44.0	12	2	AR182005	Se
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30	8.8	73.3	44.0	12	2	AR948135	Se
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C 50	12	70.6	60.0	17	2	AR597705	Se
C 51	12	70.6	60.0	17	2	AR841343	Se
C 52	12	70.6	60.0	17	2	AR841344	Se
C 53	12	70.6	60.0	17	2	AR845950	Se
C 54	12	70.6	60.0	17	2	AR845951	Se
C 55	12	70.6	60.0	17	2	AR848268	Se
C 56	8.4	70.0	42.0	12	2	AR101078	Se
C 57	8.4	70.0	42.0	12	2	CS097732	Se
C 58	8.4	70.0	42.0	12	2	CS097756	Se
C 59	8.4	70.0	42.0	12	2	CS540753	Se
C 60	8.4	70.0	42.0	12	2	I07921	Sequ
C 61	8.4	70.0	42.0	12	2	I34823	Sequ
C 62	8.4	70.0	42.0	12	2	AR893297	Se
C 63	8.4	70.0	42.0	12	2	AR893306	Se

ALIGNMENTS

RESULT 1	BD066222	14 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD066222	An antisense oligonucleotide preparation method.			
DEFINITION	BD066222	An antisense oligonucleotide preparation method.			
ACCESSION	BD066222.1	GI:22611825			
VERSION	JP 2001511000-A/857.				
KEYWORDS	unidentified				
SOURCE	unidentified				
ORGANISM	unclassified sequences.				
REFERENCE	1 (bases 1 to 14)				
AUTHORS	Schlingensiefen, K.H. and Brysch, W.				
TITLE	An antisense oligonucleotide preparation method				
JOURNAL	Patent: JP 2001511000-A 857 07-AUG-2001;				
COMMENT	BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH				
	OS Unknown				
	PN JP 2001511000-A/857				
	PD 07-AUG-2001				
	PF 30-JAN-1998 JP 1998532533				
	PI 31-JAN-1997 EP 97101531.8				
	PR KARL HERMANN SCHLINGENSIEFEN, WOLFGANG BRYSCH				
	PC C12N15/11, C07H21/04, A61K31/70				
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
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Db 2 GTTGAAGTTGCTG 14

RESULT 2
LOCUS A42517 14 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 33 from Patent WO9502051.
ACCESSION A42517
VERSION A42517.1 GI:2297966
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and
Brysch,W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND
CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 33 19-JAN-1995;
COMMENT BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
Other publication AU 7345694 950206.
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Best Local Similarity 92.3%; Pred. No. 3.2e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
|||||
Db 2 GTTGAAGTTGCTG 14

RESULT 3
LOCUS A88709 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 857 from Patent WO9833904.
ACCESSION A88709
VERSION A88709.1 GI:6737279
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 857 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 3.2e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
|||||
Db 2 GTTGAAGTTGCTG 14

RESULT 4
LOCUS AR774928 14 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 857 from patent US 6972171.
ACCESSION AR774928
VERSION AR774928.1 GI:83352192
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.-H. and Brysch,W.
TITLE Antisense oligonucleotide preparation method
JOURNAL Patent: US 6972171-A 857 06-DEC-2005;
BIOGNOSTIK Ges. fur biomolekulare Diagnostik mbH; Gottingen;
EPX;
FEATURES
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Score over Length 81.4%;
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
|||||
Db 2 GTTGAAGTTGCTG 14

DD236265 20 bp DNA linear PAT 26-APR-2005
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis accelerator and an apoptosis inhibitor.
ACCESSION DD236265.1 GI:94046395
VERSION DD236265 WO 2005093082-A/16.
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakagawara,A. and Ozaki,T.
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis accelerator and an apoptosis inhibitor
JOURNAL Patent: WO 2005093082-A 16 06-OCT-2005;
Hisamitsu Pharmaceutical Co Inc
COMMENT OS Artificial
PN WO 2005093082-A/16
PD 06-OCT-2005
PF 23-MAR-2005 WO 2005JP005247
PR 14-JUN-2004 JP 200 4-176107, 26-MAR-2004 JP 200 4-093266 PI
akira nakagawara, toshifumi ozaki
CC primer for Bax
FH Key Location/Qualifiers.
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
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Db 2 GTTGAAGTTGCTG 14

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Score over Length 80.0%;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CAGTTGAAGTTGCCGT 16

RESULT 6
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LOCUS      DD248708          20 bp DNA linear PAT 18-MAY-2006
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic
            compounds, an apoptosis accelerator and an apoptosis inhibitor.
ACCESSION  DD248708
VERSION    DD248708.1 GI:99024603
KEYWORDS   JP 2005304470-A/16.
SOURCE     unidentified
ORGANISM   unclassified sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Nakagawara,A. and Ozaki,T.
TITLE      Screening methods for pro-apoptotic compounds or anti-apoptotic
            compounds, an apoptosis accelerator and an apoptosis inhibitor
JOURNAL    Patent: JP 2005304470-A 16 04-NOV-2005;
            Hisamitsu Pharmaceutical Co Inc
COMMENT    OS Artificial
            PN JP 2005304470-A/16
            PD 04-NOV-2005
            PF 14-JUN-2004 JP 2004176107
            PI akira nakagawara,toshifumi ozaki
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Query Match      80.0%; Score 16; DB 2; Length 20;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
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Db 1 CAGTTGAAGTTGCCGT 16

RESULT 7
DD402954
LOCUS      DD402954          20 bp DNA linear PAT 21-FEB-2007
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic
            compounds, an apoptosis inhibitor.
ACCESSION  DD402954
VERSION    DD402954.1 GI:126146805
KEYWORDS   JP 2006223265-A/8.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Nakagawara,A. and Ozaki,T.
TITLE      Screening methods for pro-apoptotic compounds or anti-apoptotic

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ORIGIN
Query Match      80.0%; Score 16; DB 2; Length 20;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
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Db 1 CAGTTGAAGTTGCCGT 16

RESULT 8
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LOCUS      DD404058          20 bp DNA linear PAT 21-FEB-2007
DEFINITION Method of screening a gene related to a quantity of HCV.
ACCESSION  DD404058
VERSION    DD404058.1 GI:126149401
KEYWORDS   WO 2006085407-A/21.
SOURCE     unidentified
ORGANISM   unclassified sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Esumi,M. and Takayama,T.
TITLE      Method of screening a gene related to a quantity of HCV
JOURNAL    Patent: WO 2006085407-A 21 17-AUG-2006;
            Nihon University
COMMENT    OS Artificial
            PN WO 2006085407-A/21
            PD 17-AUG-2006
            PF 30-SEP-2005 WO 2005JP018573
            PR 09-FEB-2005 JP 05P 033707
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Score over Length 80.0%;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
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Db 1 CAGTTGAAGTTGCCGT 16

RESULT 9
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LOCUS      AR192983          15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8471 from patent US 6346398.
ACCESSION  AR192983
VERSION    AR192983.1 GI:20238948
SOURCE     AR192983.1
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 8471 12-FEB-2002;
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QY 3 CCCAGTTGAAGT 14
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RESULT 10
AR326724/c
LOCUS AR326724 15 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4126 from patent US 6566127.
ACCESSION AR326724
VERSION AR326724.1 GI:33712532
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4126 20-MAY-2003;
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
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Db 15 CCCAGTTGAAGT 4

RESULT 11
AR600184/c
LOCUS AR600184 15 bp RNA linear PAT 15-DEC-2004
DEFINITION Sequence 4126 from patent US 6818447.
ACCESSION AR600184
VERSION AR600184.1 GI:56651198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 4126 16-NOV-2004;
Sirna Therapeutics, Inc.; Boulder, CO

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or conditions related to levels of vascular endothelial growth factor receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 4126 25-APR-2006;
Sirna Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 15 CCCAGTTGAAGT 4

RESULT 12
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LOCUS AR843823 15 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 4126 from patent US 7034009.
ACCESSION AR843823
VERSION AR843823.1 GI:111931376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or conditions related to levels of vascular endothelial growth factor receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 4126 25-APR-2006;
Sirna Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES Location/Qualifiers
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Query Match 60.0%; Score 12; DB 2; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 15 CCCAGTTGAAGT 4

RESULT 13
BD376104/c
LOCUS BD376104 14 bp DNA linear PAT 04-NOV-2005
DEFINITION USING POLYAMIDE NUCLEIC ACID OLIGOMERS TO ENGENDER A BIOLOGICAL RESPONSE.
ACCESSION BD376104
VERSION BD376104.1 GI:92275004
KEYWORDS JP 2003523307-A/14.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 14)
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
TITLE Jansen,K., Hoshall,C.V., Tyler,B.M., McCormick,D.J., Cusack,B.M., Douglas,C.L. and Richelson,E.
JOURNAL USING POLYAMIDE NUCLEIC ACID OLIGOMERS TO ENGENDER A BIOLOGICAL RESPONSE
PATENT: JP 2003523307-A 14 05-AUG-2003;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH
COMMENT OS Rattus sp.
PN JP 2003523307-A/14
PD 05-AUG-2003

PF 16-OCT-1998 JP 2000516984
PR 08-OCT-1998 US 09/168791,08-OCT-1998 US 09/168519, PR
08-OCT-1998 US 09/168714,30-JAN-1998 US 09/016685, PR
17-OCT-1997 US 08/953269
PI karen jansen,clark v hoshall,beth marie tyler,daniel j PI
mccormick,
PI bernadette marie cusack,christopher lee douglas,elliott PI
richelson
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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 14 CAGATGAAGTTG 3
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AR527594/c
LOCUS 14 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 14 from patent US 6723560.
ACCESSION AR527594
VERSION AR527594.1 GI:53914707
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Richelson,E., Tyler,B.M., Cusack,B.M., Douglas,C.L. and Jansen,K.
TITLE Using polyamide nucleic acid oligomers to engender a biological response
JOURNAL Patent: US 6723560-A 14 20-APR-2004;
Mayo Foundation for Medical Education and Research; Rochester, MN
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Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 1.2e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CAGTTGAAGTTG 16
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Db 14 CAGATGAAGTTG 3
RESULT 15
AR791253/c
LOCUS 14 bp DNA linear PAT 05-APR-2006
DEFINITION Sequence 14 from patent US 6989270.
ACCESSION AR791253
VERSION AR791253.1 GI:91138201
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Richelson,E., Tyler,B.M., Cusack,B.M., Douglas,C.L. and Jansen,K.
TITLE Using polyamide nucleic acid oligomers to engender a biological response
PF 16-OCT-1998 JP 2000516984
PR 08-OCT-1998 US 09/168791,08-OCT-1998 US 09/168519, PR
08-OCT-1998 US 09/168714,30-JAN-1998 US 09/016685, PR
17-OCT-1997 US 08/953269
PI karen jansen,clark v hoshall,beth marie tyler,daniel j PI
mccormick,
PI bernadette marie cusack,christopher lee douglas,elliott PI
richelson
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Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 1.2e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CAGTTGAAGTTG 16
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Db 14 CAGATGAAGTTG 3
RESULT 14
AR527594/c
LOCUS 14 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 14 from patent US 6723560.
ACCESSION AR527594
VERSION AR527594.1 GI:53914707
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Richelson,E., Tyler,B.M., Cusack,B.M., Douglas,C.L. and Jansen,K.
TITLE Using polyamide nucleic acid oligomers to engender a biological response
JOURNAL Patent: US 6723560-A 14 20-APR-2004;
Mayo Foundation for Medical Education and Research; Rochester, MN
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Best Local Similarity 91.7%; Pred. No. 1.2e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CAGTTGAAGTTG 16
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Db 14 CAGATGAAGTTG 3
RESULT 15
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LOCUS 14 bp DNA linear PAT 05-APR-2006
DEFINITION Sequence 14 from patent US 6989270.
ACCESSION AR791253
VERSION AR791253.1 GI:91138201
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Richelson,E., Tyler,B.M., Cusack,B.M., Douglas,C.L. and Jansen,K.
TITLE Using polyamide nucleic acid oligomers to engender a biological response
JOURNAL Patent: US 6989270-A 14 24-JAN-2006;
Mayo Foundation for Medical Education and Research; Rochester, MN;
US;
FEATURES
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Query Match 52.0%; Score 10.4; DB 2; Length 14;
Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 1.2e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 14 CAGATGAAGTTG 3
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AR328405
LOCUS 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5807 from patent US 6566127.
ACCESSION AR328405
VERSION AR328405.1 GI:33714213
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5807 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
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Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCCCCAGTTGAAGTT 15
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Db 2 GACCCAGATGAAGTT 16
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AR845504
LOCUS 16 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 5807 from patent US 7034009.
ACCESSION AR845504
VERSION AR845504.1 GI:111933057
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or conditions related to levels of vascular endothelial growth factor receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 5807 25-APR-2006;
Sirta Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
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ORIGIN

Query Match 59.0%; Score 11.8; DB 2; Length 16;
 Score over Length 73.3%;
 Best Local Similarity 86.7%; Pred. No. 1.9e+05;
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QY 1 GCCCCAGTTGAAGTT 15
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 Db 2 GACCCAGATGAAGTT 16
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RESULT 18
 BD209027/c
 LOCUS 15 bp RNA linear PAT 04-NOV-2005
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
 to hepatitis C virus infection.
 ACCESSION BD209027
 VERSION BD209027.1 GI:33018797
 KEYWORDS JP 2002512791-A/2617.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE 1 (bases 1 to 15)
 AUTHORS Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
 TITLE Enzymatic nucleic acid treatment of diseases or conditions related
 to hepatitis C virus infection
 JOURNAL Patent: JP 2002512791-A 2617 08-MAY-2002;
 RIBOZYME PHARMACEUTICALS INC
 COMMENT OS Hepatitis virus (hepatitis C virus)
 PN JP 2002512791-A/2617
 PD 08-MAY-2002
 PF 26-APR-1999 JP 2000545991
 PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
 LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
 PAVCO,
 PI DENNIS MACEJAK
 PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
 A61K37/66,
 PC C12N15/00
 CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC hepatitis C virus infection.
 FH Key Location/Qualifiers
 FT source 1..15
 FT /organism='Hepatitis virus (hepatitis C FT
 virus)'. Location/Qualifiers

FEATURES

source
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 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 55.0%; Score 11; DB 2; Length 15;
 Score over Length 73.3%;
 Best Local Similarity 100.0%; Pred. No. 5.4e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAG 13
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 Db 15 CCAGTTGAAGT 5
 | | | | | | | | | |

RESULT 19

AR193008/c
 LOCUS 15 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 8496 from patent US 6346398.
 ACCESSION AR193008
 VERSION AR193008.1 GI:20238973
 KEYWORDS
 SOURCE Unknown.

ORGANISM

Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 8496 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..15
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 55.0%; Score 11; DB 2; Length 15;
 Score over Length 73.3%;
 Best Local Similarity 100.0%; Pred. No. 5.4e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
 | | | | | | | | | |
 Db 15 CCAGTTGAAGT 5
 | | | | | | | | | |

RESULT 20

AR326748/c
 LOCUS 15 bp RNA linear PAT 17-AUG-2003
 DEFINITION Sequence 4150 from patent US 6566127.
 ACCESSION AR326748
 VERSION AR326748.1 GI:33712556
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 4150 20-MAY-2003;
 RIBOZYME PHARMACEUTICALS, INC. and Chiron Corporation; Boulder, CO
 FEATURES Location/Qualifiers
 source 1..15
 /organism="unknown"
 /mol_type="unassigned RNA"

ORIGIN

Query Match 55.0%; Score 11; DB 2; Length 15;
 Score over Length 73.3%;
 Best Local Similarity 100.0%; Pred. No. 5.4e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
 | | | | | | | | | |
 Db 15 CCAGTTGAAGT 5
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RESULT 21

AR600208/c
 LOCUS 15 bp RNA linear PAT 15-DEC-2004
 DEFINITION Sequence 4150 from patent US 6818447.
 ACCESSION AR600208
 VERSION AR600208.1 GI:56651222
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6818447-A 4150 16-NOV-2004;
 Sirna Therapeutics, Inc.; Boulder, CO
 FEATURES Location/Qualifiers
 source 1..15

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/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match      55.0%; Score 11; DB 2; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14
    |||||
Db 15 CCAGTTGAAGT 5

RESULT 22
AR843847/c
LOCUS AR843847 15 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 4150 from patent US 7034009.
ACCESSION AR843847
VERSION AR843847.1 GI:111931400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 4150 25-APR-2006;
        Sirna Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
        US;
FEATURES
    source      Location/Qualifiers
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        /organism="unknown"
        /mol_type="unassigned RNA"

ORIGIN
Query Match      55.0%; Score 11; DB 2; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14
    |||||
Db 15 CCAGTTGAAGT 5

RESULT 23
BD211445
LOCUS BD211445 12 bp DNA linear PAT 04-NOV-2005
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211445
VERSION BD211445.1 GI:33021215
KEYWORDS JP 2002510492-A/14.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Ford,J. and Pace,A.
TITLE A novel interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: JP 2002510492-A 14 09-APR-2002;
        HYSEQ INC
COMMENT OS Artificial Sequence
        PN JP 2002510492-A/14
        PD 09-APR-2002
        PF 05-APR-1999 JP 2000542457
        PR 03-APR-1998 US 09/055010.15-MAY-1998 US 09/079909 PR
        20-MAY-1998 US 09/082364.19-JUN-1998 US 09/099818 PR
        31-JUL-1998 US 09/127698.13-JAN-1999 US 09/229591 PR
        17-FEB-1999 US 09/251370
        PI JOHN FORD, ANN PACE
        PC C12N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,

PC C12N1/19,
PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
C12N15/00,
PC A61K37/02,C12N5/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..12
FT /organism='Artificial Sequence'.

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        /db_xref="taxon:32630"

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Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
    |||||
Db 1 CCACAGTGAAG 12

RESULT 24
AR058661
LOCUS AR058661 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 238 from patent US 5837832.
ACCESSION AR058661
VERSION AR058661.1 GI:5984238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
        Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 238 17-NOV-1998;
        Location/Qualifiers
FEATURES
    source      Location/Qualifiers
    Qy 1..12
        /organism="unknown"
        /mol_type="unassigned DNA"

ORIGIN
Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
    |||||
Db 1 TGAAGTTGCAGT 12

RESULT 25
AR058662
LOCUS AR058662 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 239 from patent US 5837832.
ACCESSION AR058662
VERSION AR058662.1 GI:5984239
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
        Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 239 17-NOV-1998;
        Location/Qualifiers
FEATURES
    source      Location/Qualifiers
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        /organism="unknown"
        /mol_type="unassigned DNA"

ORIGIN
Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
    |||||
Db 1 TGAAGTTGCAGT 12
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Db 1 CCACAGGTGAAG 12

RESULT 28

AR221139

LOCUS 12 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 22 from patent US 6426191.

ACCESSION AR221139

VERSION AR221139.1 GI:23328024

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Ford, J. and Pace, A.

TITLE Assays involving an IL-1 receptor antagonist

JOURNAL Patent: US 6426191-A 22 30-JUL-2002;

Hyseq, Inc.; Sunnyvale, CA

FEATURES

source

1..12

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 9.2e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13

|||||

Db 1 CCACAGGTGAAG 12

RESULT 29

AR302967

LOCUS 12 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 22 from patent US 6541623.

ACCESSION AR302967

VERSION AR302967.1 GI:31691567

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.

TITLE Interleukin-1 receptor antagonist and uses thereof

JOURNAL Patent: US 6541623-A 22 01-APR-2003;

Hyseq, Inc.; Sunnyvale, CA

FEATURES

source

1..12

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 9.2e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13

|||||

Db 1 CCACAGGTGAAG 12

RESULT 30

AR948135

LOCUS 12 bp DNA linear PAT 08-OCT-2006

DEFINITION Sequence 357 from patent US 7115364.

ACCESSION AR948135

VERSION AR948135.1 GI:115839540

KEYWORDS

SOURCE Unknown.

Db 1 CCACAGGTGAAG 12

RESULT 26

EA008497

LOCUS 12 bp DNA linear PAT 06-DEC-2006

DEFINITION Sequence 32 from patent US 7122652.

ACCESSION EA008497

VERSION EA008497.1 GI:118817729

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Wojnowski, L. and Hustert, E.

TITLE Polymorphisms in the human hpxr gene and their use diagnostic and therapeutic applications

JOURNAL Patent: US 7122652-A 32 17-OCT-2006;

Location/Qualifiers

source

1..12

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 9.2e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13

|||||

Db 1 CCCAGGTGAGG 12

RESULT 27

AR182005

LOCUS 12 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 22 from patent US 6337072.

ACCESSION AR182005

VERSION AR182005.1 GI:20224921

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Ford, J. and Pace, A.

TITLE Interleukin-1 receptor antagonist and recombinant production thereof

JOURNAL Patent: US 6337072-A 22 08-JAN-2002;

Location/Qualifiers

source

1..12

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 9.2e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13

|||||

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee, M., Cronin, M.T., Fodor, S.P.A., Gingeras, T.R., Huang, X.C., Hubbell, E.A., Lipshutz, R.J., Lobb, P.E., Miyada, C.G., Morris, M.S., Shah, N., and Sheldron, E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 7115364-A 357 03-OCT-2006; Affymetrix, Inc.; Santa Clara, CA; US;

FEATURES
source Location/Qualifiers
1..12
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTCCGT 20
Db 1 TGGAGTTGCAGT 12

RESULT 31
AR948136
LOCUS AR948136 12 bp DNA linear PAT 08-OCT-2006
DEFINITION Sequence 358 from patent US 7115364.
ACCESSION AR948136
VERSION AR948136.1 GI:115839541
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee, M., Cronin, M.T., Fodor, S.P.A., Gingeras, T.R., Huang, X.C., Hubbell, E.A., Lipshutz, R.J., Lobb, P.E., Miyada, C.G., Morris, M.S., Shah, N., and Sheldron, E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 7115364-A 358 03-OCT-2006; Affymetrix, Inc.; Santa Clara, CA; US;

FEATURES
source Location/Qualifiers
1..12
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 ATTTGAGTTGC 12

RESULT 32
AX069325
LOCUS AX069325 12 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 22 from Patent WO0102571.
ACCESSION AX069325
VERSION AX069325.1 GI:12579191
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ford, J. and Pace, A.
TITLE A interleukin-1 receptor antagonist and uses thereof

JOURNAL Patent: WO 0102571-A 22 11-JAN-2001;
HYSEQ, INC. (US)
FEATURES
source Location/Qualifiers
1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Splice Acceptor Site"

ORIGIN
Query Match 44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 1 CCACAGGTGAAG 12

RESULT 33
AX098969
LOCUS AX098969 12 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 32 from Patent WO0120026.
ACCESSION AX098969
VERSION AX098969.1 GI:13538179
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wojnowski, L. and Hustert, E.
TITLE Polymorphisms in the human hpxr gene and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0120026-A 32 22-MAR-2001; Epidauros Biotechnologie AG (DE)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial sequence"

ORIGIN
Query Match 44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 1 CCCAGGTGAGG 12

RESULT 34
AX136994
LOCUS AX136994 12 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 68 from Patent EP1088900.
ACCESSION AX136994
VERSION AX136994.1 GI:14273341
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hustert, E., Wojnowski, L. and Eiselt, R.
TITLE Polymorphisms in the human cyp3a4, cyp3a7 and hpxr genes and their use in diagnostic and therapeutic applications
JOURNAL Patent: EP 1088900-A 68 04-APR-2001; Epidauros Biotechnologie AG (DE)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DNA"

ORIGIN
Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGCAAG 13
Db 1 CCCAGGTGAGG 12

RESULT 35
BD257601/c
LOCUS      17 bp      DNA      linear      PAT 04-NOV-2005
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD257601
VERSION    BD257601.1 GI:33067371
KEYWORDS  JP 2002541795-A/5394.
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE  1 (bases 1 to 17)
AUTHORS   Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE     Regulation of repressor genes using nucleic acid molecules
JOURNAL   Patent: JP 2002541795-A 5394 10-DEC-2002;
          RIBOZYME PHARMACEUTICALS INC
COMMENT   OS Eukaryote
          PN JP 2002541795-A/5394
          PD 10-DEC-2002
          PF 11-APR-2000 JP 2000611654
          PR 12-APR-1999 US 60/129390
          PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
          C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC
          C12P21/02,
          PC
          C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
          C12R1:91),
          PC
          PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
          PC A61K37/02,
          PC (C12N5/00, C12R1:91)
          CC Regulation of repressor genes using nucleic acid molecules FH
          Key Location/Qualifiers
          FT source 1..17
          /organism='Eukaryote'.
          FEATURES
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          1..17
          /organism='unidentified'
          /mol_type='unassigned DNA'
          /db_xref="taxon:32644"

ORIGIN
Query Match      62.0%; Score 12.4; DB 2; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
Db 15 CCAGTTGAAGCTGC 2

RESULT 37
BD066223
LOCUS      14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066223
VERSION    BD066223.1 GI:22611826
KEYWORDS  JP 2001511000-A/858.
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE  1 (bases 1 to 14)
AUTHORS   Schlingensiepen, K.H. and Brysch, W.
TITLE     An antisense oligonucleotide preparation method
JOURNAL   Patent: JP 2001511000-A 858 07-AUG-2001;
          BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT   OS Unknown
          PN JP 2001511000-A/858
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533
          PR 31-JAN-1997 EP 97101531.8
          PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
          PC C12N15/11, C07H21/04, A61K31/70
          CC An antisense oligonucleotide preparation method FH
          Key Location/Qualifiers
          FT source 1..14
          /organism='Unknown'.
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          /organism='unidentified'
          /mol_type='genomic DNA'
          /db_xref="taxon:32644"

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ORIGIN
Query Match          50.0%; Score 10; DB 2; Length 14;
Score over Length    71.4%;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 5 GTTGAAGTTG 14

RESULT 38
LOCUS A42518 14 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 34 from Patent WO9502051.
ACCESSION A42518
VERSION A42518.1 GI:2297967
KEYWORDS unidentified
SOURCE unclassified sequences.
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and Brysch,W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 34 19-JAN-1995;
COMMENT BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
FEATURES Other publication AU 7345694 950206.
source Location/Qualifiers
1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match          50.0%; Score 10; DB 2; Length 14;
Score over Length    71.4%;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 5 GTTGAAGTTG 14

RESULT 39
LOCUS A88710 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 858 from Patent WO9833904.
ACCESSION A88710
VERSION A88710.1 GI:6737280
KEYWORDS unidentified
SOURCE unclassified sequences.
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 858 06-AUG-1998;
COMMENT BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers
1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match          50.0%; Score 10; DB 2; Length 14;
Score over Length    71.4%;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 5 GTTGAAGTTG 14

RESULT 40
LOCUS AR774929 14 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 858 from patent US 6972171.
ACCESSION AR774929
VERSION AR774929.1 GI:83352193
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.-H. and Brysch,W.
TITLE Antisense oligonucleotide preparation method
JOURNAL Patent: US 6972171-A 858 06-DEC-2005;
COMMENT Biognostik Ges. fur biomolekulare Diagnostik mbH; Gottingen; EPX;
FEATURES Location/Qualifiers
1..14
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match          50.0%; Score 10; DB 2; Length 14;
Score over Length    71.4%;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 5 GTTGAAGTTG 14

RESULT 41
LOCUS CS508144/c 17 bp RNA linear PAT 02-APR-2007
DEFINITION Sequence 3654 from Patent EP1767632.
ACCESSION CS508144
VERSION CS508144.1 GI:138751678
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Escobedo,J., Pavco,P., Sandburg,J., McSwiggen,J., Stinchcomb,D. and Gordon,G.
TITLE A method for local administration of synthetic double-stranded oligonucleotides targeting a VEGF receptor
JOURNAL Patent: EP 1767632-A 3654 28-MAR-2007;
COMMENT Sirna Therapeutics, Inc. (US); Novartis Vaccines and Diagnostics, Inc. (US)
FEATURES Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Query Match          60.0%; Score 12; DB 2; Length 17;
Score over Length    70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 3 CCCAGTTGAAGT 14

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Db      14  CCCAGTTGAAGT 3

RESULT 42
DD126995/c
LOCUS      DD126995      17 bp      RNA      linear      PAT 04-NOV-2005
DEFINITION NUCLEIC ACID BASED MODULATION OF FEMALE REPRODUCTIVE DISEASES AND
CONDITIONS.
ACCESSION  DD126995
VERSION     DD126995.1 GI:92886729
KEYWORDS   JP 2005500025-A/3654.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
            Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Gordon,J., Sandberg,J., Stinchcomb,D., Pavco,P., Mcswiggen,J. and
            Escobedo,J.
TITLE     NUCLEIC ACID BASED MODULATION OF FEMALE REPRODUCTIVE DISEASES AND
CONDITIONS
JOURNAL    Patent: JP 2005500025-A 3654 06-JAN-2005;
            SIRNA THERAPEUTICS INC, CHIRON CORP
COMMENT    OS Homo Sapiens
            PN JP 2005500025-A/3654
            PD 06-JAN-2005
            PF 29-MAY-2002 JP 2003500106
            PR 09/870161,30-NOV-2001 US 60/334461, PR
            PI 03-MAY-2002 US 10/138674
            PI Jirardo gordon,jennifer sandberg,dan stinchcomb,pamela pavco,
            PI james mcswiggen,jaime escobedo
            CC
            FH Key Location/Qualifiers.
FEATURES   source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3  CCCAGTTGAAGT 14
Db      14  CCCAGTTGAAGT 3

RESULT 43
AR188391/c
LOCUS      AR188391      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 3879 from patent US 6346398.
ACCESSION  AR188391
VERSION     AR188391.1 GI:20234356
KEYWORDS   Patent: US 6346398-A 3879 12-FEB-2002;
            Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6346398-A 3879 12-FEB-2002;
            Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES   source
            1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3  CCCAGTTGAAGT 14
Db      14  CCCAGTTGAAGT 3

RESULT 44
AR188392/c
LOCUS      AR188392      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 3880 from patent US 6346398.
ACCESSION  AR188392
VERSION     AR188392.1 GI:20234357
KEYWORDS   Patent: US 6346398-A 3880 12-FEB-2002;
            related to levels of vascular endothelial growth factor receptor
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6346398-A 3880 12-FEB-2002;
            related to levels of vascular endothelial growth factor receptor
FEATURES   source
            1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3  CCCAGTTGAAGT 14
Db      16  CCCAGTTGAAGT 5

RESULT 45
AR324244/c
LOCUS      AR324244      17 bp      RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1646 from patent US 6566127.
ACCESSION  AR324244
VERSION     AR324244.1 GI:33710052
KEYWORDS   Patent: US 6566127-A 1646 20-MAY-2003;
            Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 1646 20-MAY-2003;
            Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES   source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

ORIGIN
Query Match      60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3  CCCAGTTGAAGT 14
Db      17  CCCAGTTGAAGT 6

RESULT 46
AR324245/c
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LOCUS AR324245 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1647 from patent US 6566127.
ACCESSION AR324245
VERSION AR324245.1 GI:33710053
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1647 20-MAY-2003;
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 CCCAGTTGAAGT 14
|||||
Db 16 CCCAGTTGAAGT 5
RESULT 47
AR328851/c
LOCUS AR328851 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6253 from patent US 6566127.
ACCESSION AR328851
VERSION AR328851.1 GI:33714659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6253 20-MAY-2003;
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 CCCAGTTGAAGT 14
|||||
Db 15 CCCAGTTGAAGT 4
RESULT 48
AR328852/c
LOCUS AR328852 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6254 from patent US 6566127.
ACCESSION AR328852
VERSION AR328852.1 GI:33714660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)

LOCUS AR324245 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1647 from patent US 6566127.
ACCESSION AR324245
VERSION AR324245.1 GI:33710053
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1647 20-MAY-2003;
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 CCCAGTTGAAGT 14
|||||
Db 12 CCCAGTTGAAGT 1
RESULT 49
AR597704/c
LOCUS AR597704 17 bp RNA linear PAT 15-DEC-2004
DEFINITION Sequence 1646 from patent US 6818447.
ACCESSION AR597704
VERSION AR597704.1 GI:56648718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 1646 16-NOV-2004;
Sirna Therapeutics, Inc.; Boulder, CO
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 CCCAGTTGAAGT 14
|||||
Db 17 CCCAGTTGAAGT 6
RESULT 50
AR597705/c
LOCUS AR597705 17 bp RNA linear PAT 15-DEC-2004
DEFINITION Sequence 1647 from patent US 6818447.
ACCESSION AR597705
VERSION AR597705.1 GI:56648719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 1647 16-NOV-2004;
Sirna Therapeutics, Inc.; Boulder, CO
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"


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ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 16 CCCAGTTGAAGT 5

RESULT 51
LOCUS AR841343 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 1646 from patent US 7034009.
ACCESSION AR841343
VERSION AR841343.1 GI:111928896
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 1646 25-APR-2006;
Sirma Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 17 CCCAGTTGAAGT 6

RESULT 52
LOCUS AR841344/c 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 1647 from patent US 7034009.
ACCESSION AR841344
VERSION AR841344.1 GI:111928897
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 1647 25-APR-2006;
Sirma Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 12 CCCAGTTGAAGT 1

RESULT 53
LOCUS AR845950/c 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 6253 from patent US 7034009.
ACCESSION AR845950
VERSION AR845950.1 GI:111933503
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 6253 25-APR-2006;
Sirma Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 54
LOCUS AR845951/c 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 6254 from patent US 7034009.
ACCESSION AR845951
VERSION AR845951.1 GI:111933504
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 6254 25-APR-2006;
Sirma Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 12 CCCAGTTGAAGT 1
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RESULT 55
LOCUS AR848268/c 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 8571 from patent US 7034009.
ACCESSION AR848268
VERSION AR848268.1 GI:111935821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Eacobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 8571 25-APR-2006;
US; Sirna Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;

FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 14 CCCAGTTGAAGT 3

RESULT 56
LOCUS AR101078/c 12 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 48 from patent US 6083694.
ACCESSION AR101078
VERSION AR101078.1 GI:12811876
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hardy,J. and Goate,A.M.
TITLE Method for elucidation and detection of polymorphisms, splice
variants, and proximal coding mutations using intronic sequences of
the alzheimer's S182 gene
JOURNAL Patent: US 6083694-A 48 04-JUL-2000;
US;

FEATURES
source Location/Qualifiers
1..12
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAGTTG 16
Db 10 GTTGATGTTG 1

RESULT 57
LOCUS CS097732/c 12 bp DNA linear PAT 03-JUN-2005
DEFINITION Sequence 5 from Patent EP1500329.
ACCESSION CS097732

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VERSION CS097732.1 GI:66954134
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Green,L., Jakobovits,A., Klapholz,S., Kucherlapati,R. and Mendez,M.
TITLE Transgenic mammals having human Ig loci including plural VH and
Vkappa regions and antibodies produced therefrom
JOURNAL Patent: EP 1500329-A 5 26-JAN-2005;
US; Abgenix, Inc. (US)
FEATURES
source Location/Qualifiers
1..12
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTG 10
Db 12 GCCCCAGTAG 3

RESULT 58
LOCUS CS097756/c 12 bp DNA linear PAT 03-JUN-2005
DEFINITION Sequence 29 from Patent EP1500329.
ACCESSION CS097756
VERSION CS097756.1 GI:66954158
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Green,L., Jakobovits,A., Klapholz,S., Kucherlapati,R. and Mendez,M.
TITLE Transgenic mammals having human Ig loci including plural VH and
Vkappa regions and antibodies produced therefrom
JOURNAL Patent: EP 1500329-A 29 26-JAN-2005;
US; Abgenix, Inc. (US)
FEATURES
source Location/Qualifiers
1..12
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTG 10
Db 12 GCCCCAGTAG 3

RESULT 59
LOCUS CS540753/c 12 bp DNA linear PAT 20-APR-2007
DEFINITION Sequence 132 from Patent WO2007012576.
ACCESSION CS540753
VERSION CS540753.1 GI:145581914
KEYWORDS
SOURCE unidentified

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ORGANISM      unidentified
unclassified sequences.
REFERENCE      1
AUTHORS        Zank, T. and Oswald, O.
TITLE          Combination of lipid metabolism proteins and uses thereof
JOURNAL        Patent: WO 2007012576-A 132 01-FEB-2007;
               BASF Plant Science GmbH (DE)
FEATURES       Location/Qualifiers
               1..12
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
               /note="Unidentified"

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 AGTTGAGTTGTC 17
       ||:|||||
Db      12 AGYTGAGTTGTC 1

RESULT 60
LOCUS      I07921
DEFINITION Sequence 33 from Patent EP 0159123.
ACCESSION  I07921
VERSION     I07921.1 GI:589374
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Hsiung,H.M., Schoner,R.G. and Schoner,B.E.
TITLE        Vectors for expressing bovine growth hormone derivatives
JOURNAL      Patent: EP 0159123-A2 33 23-OCT-1985;
               Location/Qualifiers
               1..12
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GAAGTTGCCG 19
       |||:|||||
Db      12 GAAGTTGTCG 3

RESULT 61
LOCUS      I34823
DEFINITION Sequence 16 from patent US 5599673.
ACCESSION  I34823
VERSION     I34823.1 GI:2087791
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Keating,M.T., Curran,M.E. and Wang,Q.
TITLE        Long QT syndrome Genes
JOURNAL      Patent: US 5599673-A 16 04-FEB-1997;
               Location/Qualifiers
               1..12
               /organism="unknown"
               /mol_type="unassigned DNA"

FEATURES       source

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GAAGTTGCCG 19
       |||:|||||
Db      12 GAAGTTGTCG 3

RESULT 62
LOCUS      AR893297/c
DEFINITION Sequence 50 from patent US 7064244.
ACCESSION  AR893297
VERSION     AR893297.1 GI:112050376
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Jakobovits,A., Kucherlapati,R., Klapholz,S., Mendez,M.J. and
               Green,L.
TITLE        Transgenic mammals having human Ig loci including plural VH and VK
               regions and antibodies produced therefrom
JOURNAL      Patent: US 7064244-A 50 20-JUN-2006;
               Abgenix, Inc.; Fremont, CA;
               US;
               Location/Qualifiers
               1..12
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTG 10
       |||:|||||
Db      12 GCCCCAGTAG 3

RESULT 63
LOCUS      AR893306/c
DEFINITION Sequence 59 from patent US 7064244.
ACCESSION  AR893306
VERSION     AR893306.1 GI:112050389
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Jakobovits,A., Kucherlapati,R., Klapholz,S., Mendez,M.J. and
               Green,L.
TITLE        Transgenic mammals having human Ig loci including plural VH and VK
               regions and antibodies produced therefrom
JOURNAL      Patent: US 7064244-A 59 20-JUN-2006;
               Abgenix, Inc.; Fremont, CA;
               US;
               Location/Qualifiers
               1..12
               /organism="unknown"
               /mol_type="genomic DNA"

FEATURES       source

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTG 10
       |||:|||||
Db      12 GCCCCAGTAG 3

RESULT 64
LOCUS      AR893306/c
DEFINITION Sequence 59 from patent US 7064244.
ACCESSION  AR893306
VERSION     AR893306.1 GI:112050389
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Jakobovits,A., Kucherlapati,R., Klapholz,S., Mendez,M.J. and
               Green,L.
TITLE        Transgenic mammals having human Ig loci including plural VH and VK
               regions and antibodies produced therefrom
JOURNAL      Patent: US 7064244-A 59 20-JUN-2006;
               Abgenix, Inc.; Fremont, CA;
               US;
               Location/Qualifiers
               1..12
               /organism="unknown"
               /mol_type="genomic DNA"

FEATURES       source

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTG 10
       |||:|||||
Db      12 GCCCCAGTAG 3

RESULT 65
LOCUS      AR893306/c
DEFINITION Sequence 59 from patent US 7064244.
ACCESSION  AR893306
VERSION     AR893306.1 GI:112050389
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Jakobovits,A., Kucherlapati,R., Klapholz,S., Mendez,M.J. and
               Green,L.
TITLE        Transgenic mammals having human Ig loci including plural VH and VK
               regions and antibodies produced therefrom
JOURNAL      Patent: US 7064244-A 59 20-JUN-2006;
               Abgenix, Inc.; Fremont, CA;
               US;
               Location/Qualifiers
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               /organism="unknown"
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FEATURES       source

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTG 10
       |||:|||||
Db      12 GCCCCAGTAG 3
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTG 10

Db 12 GCCCCAGTAG 3

Search completed: December 3, 2007, 17:42:36
Job time : 2640 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:03:06 : Search time 8518 Seconds
(without alignments)
182.695 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagttgaagttgcgt 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 66588504 seqs, 38904969350 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570288

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_hc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_est13:*
- 12: gb_est12:*
- 13: gb_est11:*
- 14: gb_est10:*
- 15: gb_gss1:*
- 16: gb_gss2:*
- 17: gb_gss3:*
- 18: gb_gss4:*
- 19: gb_gss5:*
- 20: gb_gss6:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	14	70.0	34	12	EH339462	EH339462 192096_29
c 2	13	65.0	46	1	AI026096	AI026096 ov94h09's
c 3	12	60.0	35	15	BH861691	BH861691 SALK_0878
c 4	12	60.0	35	18	ED597720	ED597720 SALK_0878
c 5	12	60.0	41	18	E1637387	E1637387 wang-VSVG
c 6	12	60.0	47	16	BZ767445	BZ767445 SALK_1388
c 7	11	55.0	28	17	DX593658	DX593658 Lewinski-
c 8	11	55.0	30	15	BH847383	BH847383 SALK_0531
c 9	11	55.0	32	17	CZ466560	CZ466560 C00562-3p
c 10	11	55.0	37	17	DX935836	DX935836 NEI_segme
c 11	11	55.0	47	7	AV578677	AV578677 AV578677
c 12	11	55.0	47	12	EG532751	EG532751 R1X4a42d
c 13	11	55.0	50	1	AU107927	AU107927 AU107927

14	11	55.0	50	14	DR979367	DR979367 SM014218
15	10	50.0	15	12	EH308710	EH308710 016929_32
c 16	10	50.0	19	18	E1596228	E1596228 Wang-VSVG
c 17	10	50.0	20	18	E1602830	E1602830 Wang-VSVG
c 18	10	50.0	21	11	EW471844	EW471844 r1ms3601b
c 19	10	50.0	22	11	EW623052	EW623052 r1b0111
c 20	10	50.0	24	18	E1599377	E1599377 Wang-VSVG
c 21	10	50.0	26	11	EW549125	EW549125 rain08_01
c 22	10	50.0	26	15	AZ361612	AZ361612 IM0106E18
c 23	10	50.0	28	12	EH306286	EH306286 000504_34
c 24	10	50.0	28	15	BH011467	BH011467 BG02165-5
c 25	10	50.0	28	18	E1618163	E1618163 Wang-VSVG
c 26	10	50.0	30	17	CZ476737	CZ476737 d09425-5p
c 27	10	50.0	30	18	E1525731	E1525731 Wang-VSVG
c 28	10	50.0	31	1	AA993748	AA993748 ot65e02.s
c 29	10	50.0	31	19	BX947252	BX947252 Arabidops
c 30	10	50.0	32	11	EW319155	EW319155 r1in34_h1
c 31	10	50.0	32	18	E1658957	E1658957 Wang-VSVG
c 32	10	50.0	34	18	E1609128	E1609128 Wang-VSVG
c 33	10	50.0	35	12	EH338546	EH338546 192331_28
c 34	10	50.0	36	15	AZ350375	AZ350375 IM0087G22
c 35	10	50.0	37	11	EW031990	EW031990 r1ct20_f1
c 36	10	50.0	38	11	EW607208	EW607208 r1ct0233_g
c 37	10	50.0	38	18	E1558107	E1558107 Wang-VSVG
c 38	10	50.0	39	12	EC606644	EC606644 latexY04H
c 39	10	50.0	39	12	EH331535	EH331535 149871_07
c 40	10	50.0	39	14	DT011957	DT011957 VVH024H01
c 41	10	50.0	39	18	E1538658	E1538658 Wang-VSVG
c 42	10	50.0	40	1	AI097270	AI097270 qb88e05.x
c 43	10	50.0	40	18	E1538250	E1538250 Wang-VSVG
c 44	10	50.0	40	18	E1639555	E1639555 Wang-VSVG
c 45	10	50.0	41	1	AU013289	AU013289 AU013289

ALIGNMENTS

RESULT 1
EH339462/c
LOCUS: EH339462 34 bp mRNA linear EST 01-MAR-2007
DEFINITION: 192096_2950_2002 3' ESTs from HeLa cell Homo sapiens cDNA 3', mRNA
sequence.
ACCESSION: EH339462
VERSION: EH339462.1 GI:136408936
KEYWORDS: EST.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Catarrhini; Homnidae; Homo.
1 (bases 1 to 34)
Wu, O., Kim, Y.C. and Wang, S.M.
3' ESTs from HeLa cell
Unpublished (2006)
Contact: San Ming Wang
Center for Functional Genomics
ENH Research Institute, Northwestern University
1001 University Place, Evanston, IL 60201, USA
Tel: 224 364 7491
Fax: 224 364 5003
Email: swang@northwestern.edu.

FEATURES
Location/Qualifiers
1..34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Female"
/cell_line="HeLa"
/clone_lib="3' ESTs from HeLa cell"
/note="3' EST from cytoplasmic mRNA of HeLa cell collected
by 454 pyrosequencing system"

ORIGIN

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

source

1. .35
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="SALK_087845.54.25.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 60.0%; Score 12; DB 18; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.1e+04; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0;

Qy 6 AGTTGAAGTTGC 17

|||||

Db 11 AGTTGAAGTTGC 22

RESULT 5

EI637387/c

LOCUS

DEFINITION Wang-VSVGgfp-Jurkat-454-Mse-090835.2696.0476 linear GSS 25-APR-2007
Wang-VSVGgfp-Jurkat-454-Mse Homo sapiens genomic, genomic survey sequence.

ACCESSION

EI637387

VERSION

EI637387.1

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Wang, G.F., Cluffi, A., Leipig, J., Berry, C.C. and Bushman, F.D.

AUTHORS

TITLE

pyrosequencing reveals association with epigenetic modifications

JOURNAL

Genome Res. 17 (2007) In press

COMMENT

Contact: Bushman, F.D.

Department of Microbiology

University of Pennsylvania School of Medicine

402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA

19104-6076, USA

Tel: 215 573 8732

Fax: 215 573 4856

Email: bushman@mail.med.upenn.edu

Class: PCR fragment.

Location/Qualifiers

source

1. .41

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/cell_type="Jurkat"

/clone_lib="Wang-VSVGgfp-Jurkat-454-Mse"

/note="Site 1: MseI; Amplified PCR products were directly sequenced using pyrosequencing as implemented by 454 Life Sciences. An HIV-based vector transducing GFP and pseudotyped with VSV-G envelope was used."

ORIGIN

Query Match 60.0%; Score 12; DB 18; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17

|||||

Db 12 AGTTGAAGTTGC 1

RESULT 6

BZ767445

LOCUS

DEFINITION

BZ767445

Arabis thaliana genomic clone SALK_138868.42.60.x, genomic survey sequence.

ACCESSION

BZ767445

VERSION

BZ767445.1

KEYWORDS

GSS.

SOURCE

Arabis thaliana (thale cress)

ORGANISM

Arabis thaliana

REFERENCE

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

AUTHORS

Gadgil, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J., and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At2g37810.

Class: TDNA tagged.

Location/Qualifiers

source

1. .47

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

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/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 60.0%; Score 12; DB 16; Length 47;

Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16

|||||

Db 4 CAGTTGAAGTTG 15

RESULT 7

DX593658

LOCUS DX593658 28 bp DNA linear GSS 28-FEB-2007
DEFINITION Lewinski-HIVchimera-HeLa-MLVGagPuro-21D11.rev HIVMgag MLV/HIV chimera integration site Library Homo sapiens genomic, genomic survey sequence.

ACCESSION DX593658
VERSION DX593658.1 GI:98980491
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Lewinsky, M.K., Yamashita, M., Emerman, M., Ciuffi, A., Marshall, H., Crawford, G., Collins, P., Shinn, P., Leipzig, J., Hannehalli, S., Berty, C.C., Ecker, J.R. and Bushman, P.D.
TITLE Retroviral DNA integration: viral and cellular determinants of target-site selection
JOURNAL PLoS Pathog. 2 (6), e60 (2006)
PUBMED 16789841
COMMENT Contact: Bushman PD
Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
Class: shotgun.

FEATURES
source
1..28
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/cell_line="HeLa"
/clone_lib="HIVMgag MLV/HIV chimera integration site Library"
/note="HeLa cells were infected with an HIV-based chimeric virus with MLV MA, p12 and CA substituted for HIV MA and CA and the puromycin resistance gene in place of nef. Cells were selected with puromycin for 2 weeks. Genomic DNA was extracted, digested with MseI, and ligated to a linker. Viral-host DNA junctions were amplified by nested PCR and cloned into TOPO TA vectors."

ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTT 15
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Db 17 CAGTTGAAGTT 27

RESULT 8
BH847383/c
LOCUS
DEFINITION SALK 053111.20.10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_053111.20.10.x, genomic survey sequence.

ACCESSION BH847383
VERSION BH847383.1 GI:21418254
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 30)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

LOCUS DX593658 28 bp DNA linear GSS 28-FEB-2007
DEFINITION Lewinski-HIVchimera-HeLa-MLVGagPuro-21D11.rev HIVMgag MLV/HIV chimera integration site Library Homo sapiens genomic, genomic survey sequence.

ACCESSION DX593658
VERSION DX593658.1 GI:98980491
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Lewinsky, M.K., Yamashita, M., Emerman, M., Ciuffi, A., Marshall, H., Crawford, G., Collins, P., Shinn, P., Leipzig, J., Hannehalli, S., Berty, C.C., Ecker, J.R. and Bushman, P.D.
TITLE Retroviral DNA integration: viral and cellular determinants of target-site selection
JOURNAL PLoS Pathog. 2 (6), e60 (2006)
PUBMED 16789841
COMMENT Contact: Bushman PD
Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
Class: shotgun.

FEATURES
source
1..28
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/cell_line="HeLa"
/clone_lib="HIVMgag MLV/HIV chimera integration site Library"
/note="HeLa cells were infected with an HIV-based chimeric virus with MLV MA, p12 and CA substituted for HIV MA and CA and the puromycin resistance gene in place of nef. Cells were selected with puromycin for 2 weeks. Genomic DNA was extracted, digested with MseI, and ligated to a linker. Viral-host DNA junctions were amplified by nested PCR and cloned into TOPO TA vectors."

ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTT 15
|||||
Db 17 CAGTTGAAGTT 27

RESULT 8
BH847383/c
LOCUS
DEFINITION SALK 053111.20.10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_053111.20.10.x, genomic survey sequence.

ACCESSION BH847383
VERSION BH847383.1 GI:21418254
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 30)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atg27080.
Class: TDNA tagged.
Location/Qualifiers
1..30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_053111.20.10.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 55.0%; Score 11; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCG 19
|||||
Db 17 TGAAGTTGCCG 7

RESULT 9
CZ466560/c
LOCUS
DEFINITION C00562-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.

ACCESSION CZ466560
VERSION CZ466560.1 GI:62960573
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 32)
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartouni, J.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.


```

EGS32751.1 GI:116520154
EST.
Rutilus rutilus (roach minnow)
Rutilus rutilus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rutilus.
REFERENCE
1 (bases 1 to 47)
AUTHORS
Chatziandreou,N., Williams,D., Li,W., Lange,A., Chidgey,L.,
Tyler,C.R. and Cossins,A.R.
TITLE
Endocrine disruption in roach
JOURNAL
Unpublished (2007)
COMMENT
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liverpool.ac.uk
Vector has been trimmed from this EST.
Plate: 42 row: d column: 22
Seq primer: pTriplex2 5' LD 3' LD
High quality sequence stop: 47.
FEATURES
Location/Qualifiers
1..47
/organism="Rutilus rutilus"
/mol_type="mRNA"
/db_xref="taxon:48668"
/clone="42d22"
/sex="Male"
/clone_lib="250DPH (.)"
/notes="Organ: Gonade; Vector: pTriplex2; Site 1: Sf1l
GGCATTAGGCC; Site 2: Sf1l GGCCTCGGCC; cDNA library
prepared from roach 250dph (days post hatch) exposed
(exposed to EDCs)"
ORIGIN
Query Match 55.0%; Score 11; DB 12; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGTTGCCCT 20
|||||
DB 32 GAAGTTGCCCT 22

RESULT 13
AUI07927
LOCUS
AUI07927 Sugano Homo sapiens cDNA library EST 17-APR-2006
DEFINITION
ZRV61994 5', mRNA sequence.
ACCESSION
AUI07927
VERSION
AUI07927.1 GI:13557449
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Cathartini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
ENBO Rep. 2 (5), 388-393 (2001)
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5343

EGS32751.1 GI:116520154
EST.
Rutilus rutilus (roach minnow)
Rutilus rutilus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rutilus.
REFERENCE
1 (bases 1 to 47)
AUTHORS
Chatziandreou,N., Williams,D., Li,W., Lange,A., Chidgey,L.,
Tyler,C.R. and Cossins,A.R.
TITLE
Endocrine disruption in roach
JOURNAL
Unpublished (2007)
COMMENT
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liverpool.ac.uk
Vector has been trimmed from this EST.
Plate: 42 row: d column: 22
Seq primer: pTriplex2 5' LD 3' LD
High quality sequence stop: 47.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:48668"
/clone="42d22"
/sex="Male"
/clone_lib="250DPH (.)"
/notes="Organ: Gonade; Vector: pTriplex2; Site 1: Sf1l
GGCATTAGGCC; Site 2: Sf1l GGCCTCGGCC; cDNA library
prepared from roach 250dph (days post hatch) exposed
(exposed to EDCs)"
ORIGIN
Query Match 55.0%; Score 11; DB 12; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGTTGCCCT 20
|||||
DB 32 GAAGTTGCCCT 22

RESULT 13
AUI07927
LOCUS
AUI07927 Sugano Homo sapiens cDNA library EST 17-APR-2006
DEFINITION
ZRV61994 5', mRNA sequence.
ACCESSION
AUI07927
VERSION
AUI07927.1 GI:13557449
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Cathartini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
ENBO Rep. 2 (5), 388-393 (2001)
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5343

```

Matches 11; . Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAA 12
|||||
Db 21 CCCAGTTGAA 31

RESULT 15
EH308710
LOCUS EH308710 15 bp mRNA linear EST 01-MAR-2007
DEFINITION 016929_3219_3561 3' ESTs from HeLa cell Homo sapiens cDNA 3', mRNA
sequence.
ACCESSION EH308710
VERSION EH308710
KEYWORDS EST
SOURCE EH308710.1 GI:126373552
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 15)
Wu, Q., Kim, Y.-C. and Wang, S.-M.
3' ESTs from HeLa cell
Unpublished (2006)
Contact: San Ming Wang
Center for Functional Genomics
ENH Research Institute, Northwestern University
1001 University Place, Evanston, IL 60201, USA
Tel: 224 364 7491
Fax: 224 364 5003
Email: swangl@northwestern.edu.

FEATURES
source
1..15
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/cell_line="HeLa"
/clone_lib="3' ESTs from HeLa cell"
/note="3' EST from cytoplasmic mRNA of HeLa cell collected
by 454 pyrosequencing system"

ORIGIN

Query Match 50.0%; Score 10; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCC 18
|||||
Db 3 TGAAGTTGCC 12

Search completed: December 3, 2007, 18:25:11
Job time : 8525 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:01:39 ; Search time 1236 Seconds
(without alignments)
174.683 Million cell updates/sec

Title: US-10-728-509-64
Perfect score: 20
Sequence: 1 gccccagttgaagtgcgcgt 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 9073515 seqs, 5397694045 residues

Word size : 1
Total number of hits satisfying chosen parameters: 9333772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

- Database :
- 1: N_Geneseq_200711.*
 - 2: Geneseqn1980s.*
 - 3: Geneseqn2000.*
 - 4: Geneseqn2001a.*
 - 5: Geneseqn2001b.*
 - 6: Geneseqn2002a.*
 - 7: Geneseqn2002b.*
 - 8: Geneseqn2003a.*
 - 9: Geneseqn2003b.*
 - 10: Geneseqn2003c.*
 - 11: Geneseqn2003d.*
 - 12: Geneseqn2004a.*
 - 13: Geneseqn2004b.*
 - 14: Geneseqn2004c.*
 - 15: Geneseqn2004d.*
 - 16: Geneseqn2005a.*
 - 17: Geneseqn2005b.*
 - 18: Geneseqn2005c.*
 - 19: Geneseqn2006a.*
 - 20: Geneseqn2006b.*
 - 21: Geneseqn2006c.*
 - 22: Geneseqn2007.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	20	100.0	20	ADA20891	Ada20891 Human BAX
2	18	90.0	20	ADA20892	Ada20892 Human BAX
c 3	17	85.0	22	ABV73748	ABV73748 Human Bax
4	17	85.0	24	AEJ10477	AEJ10477 Target nu
5	17	85.0	24	AEJ10484	AEJ10484 Target nu
c 6	17	85.0	42	AEJ10483	AEJ10483 Circulariz
c 7	17	85.0	44	AEJ10476	AEJ10476 Circulariz
c 8	17	85.0	44	AEJ10482	AEJ10482 Circulari
c 9	17	85.0	45	AEJ10475	AEJ10475 PGR probe
10	16	80.0	20	ABX13068	ABX13068 Human bax
11	16	80.0	20	ADA20946	Ada20946 Mouse BAX

12	16	80.0	20	17	ABD12216	Aed12216 Bax (huma
13	16	80.0	20	19	AEJ97326	Aej97326 RT-PCR pr
14	16	80.0	20	19	AEK58344	Aek58344 Interfero
c 15	16	80.0	22	19	AEH24548	Aeh24548 BAX gene
c 16	16	80.0	22	19	AEH24560	Aeh24560 BAX forwa
c 17	16	80.0	22	19	AEJ10474	Aej10474 Antisense
18	15	75.0	18	8	ADA20832	Ada20832 Human BCL
19	15	75.0	25	20	AFZ227061	Afz227061 Saccharom
20	15	75.0	25	21	AGC11439	Agc11439 Saccharom
c 21	14	70.0	25	17	AED15910	Aed15910 P. putida
c 22	14	70.0	37	2	AAV85651	Aav85651 LRP5 exon
c 23	13	65.0	20	6	ABZ31305	Abz31305 Candida a
24	13	65.0	20	8	ADA20945	Ada20945 Mouse BAX
25	13	65.0	20	8	ADA20947	Ada20947 Mouse BAX
c 26	13	65.0	25	13	ABO20836	Abo20836 Mouse gen
c 27	13	65.0	25	17	AEX92152	Aex92152 Mouse gen
28	13	65.0	25	20	AFZ81835	Afz81835 Saccharom
29	13	65.0	25	21	AGC66213	Agc66213 Saccharom
30	13	65.0	29	10	ADK17509	Adk17509 SB varian
c 31	13	65.0	50	6	ABZ05963	Abz05963 Human leu
c 32	13	65.0	50	6	ABZ06328	Abz06328 Human leu
c 33	13	65.0	50	19	AFG04299	Afg04299 SNP found
c 34	12	60.0	15	2	AAV75721	Aav75721 Human flt
c 35	12	60.0	17	2	AAV71130	Aav71130 Human KDR
c 36	12	60.0	17	2	AAV71129	Aav71129 Human KDR
c 37	12	60.0	17	8	ABE61076	Abe61076 Human VEG
c 38	12	60.0	19	19	AEK84167	Aek84167 Human MMP
39	12	60.0	19	19	AEK84373	Aek84373 Human MMP
c 40	12	60.0	20	4	AAH26103	Aah26103 VEGF rece
c 41	12	60.0	21	13	ADQ93237	Adq93237 3-alpha-h
c 42	12	60.0	21	13	ADQ93231	Adq93231 3-alpha-h
43	12	60.0	21	13	ADQ93236	Adq93236 3-alpha-h
c 44	12	60.0	21	13	ADQ93232	Adq93232 3-alpha-h
c 45	12	60.0	21	13	ADQ93235	Adq93235 3-alpha-h

ALIGNMENTS

RESULT 1

ID	ADA20891	standard; DNA; 20 BP.
XX		
AC	ADA20891;	
XX		
DT	20-NOV-2003	(first entry)
XX		
DE	Human BAX	chimeric phosphorothioate oligonucleotide SEQ ID NO:64.
XX		
KW	BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;	
KW	anticonvulsant; ophthalmological; antidiabetic; virucide;	
KW	antisense therapy; BAX antagonist; BAX inhibitor;	
KW	familial amyotrophic lateral sclerosis; Alzheimer's disease;	
KW	Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;	
KW	diabetes-associated ocular disorder; scrapie infection;	
KW	aberrant apoptosis; human; phosphorothioate; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/tag= b
FT		/mod_base= OTHER
FT		/note= "phosphorothioate linkages, and all cytidine residues are 5-methylcytidines"
FT	modified_base	1..5
FT		/tag= a
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
FT	modified_base	16..20
FT		/tag= c
FT		/mod_base= OTHER

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FT      /note= "2'-O-methoxyethyls"
XX      WO2003008543-A2.
XX      30-JAN-2003.
XX      13-JUL-2002; 2002WO-US022417.
XX      17-JUL-2001; 2001US-00908147.
XX      (ISIS-) ISIS PHARM INC.
XX      Zhang H, Watt AT;
XX      WPI; 2003-239321/23.
XX      New antisense compounds, useful for modulating the expression of BCL2-
XX      associated X (BAX) protein or for treating a disease or condition
XX      associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
XX      or Alzheimer's disease.
XX      Claim 3; Page 86; 139pp; English.
XX      The present invention describes a compound (I) 8-50 nucleobases in length
XX      targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
XX      protein, where the compound specifically hybridises with the nucleic acid
XX      molecule encoding BAX protein and inhibits the expression of BAX protein.
XX      The compound specifically hybridises with at least 8-nucleobase portion
XX      of an active site on a nucleic acid molecule encoding BAX protein. Also
XX      described: (1) a composition comprising (I) and a pharmaceutical carrier
XX      or diluent; (2) inhibiting the expression of BAX protein in cells or
XX      tissues comprising contacting the cells or tissues with (I); and (3)
XX      treating an animal having a disease or condition associated with BAX
XX      protein comprising administering to the animal (I) so that expression of
XX      BAX protein is inhibited. (I) has neurotropic, neuroprotective,
XX      antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
XX      virucide activities, and can be used in antisense therapy, and as a BAX
XX      antagonist. The antisense compounds (I) are useful for modulating the
XX      expression of BAX protein, and for treating a disease or condition
XX      associated with BAX protein, e.g. familial amyotrophic lateral
XX      sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
XX      cartilage-hair hyperplasia, diabetes-associated ocular disorders or
XX      scrapie infection, or a condition that arises from aberrant apoptosis.
XX      The compounds are useful as research reagents and in diagnostics. The
XX      present sequence represents a human BAX chimeric phosphorothioate
XX      oligonucleotide, which is used in an example from the present invention.
XX      Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX      Query Match 100.0%; Score 20; DB 8; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 0.15;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCCCAGTTGAAGTTCGGT 20
Db      1 GCCCAGTTGAAGTTCGGT 20
RESULT 2
ADA20892
ID      ADA20892 standard; DNA; 20 BP.
XX      ADA20892;
XX      ADA20892;
XX      20-NOV-2003 (first entry)
XX      Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:65.
XX      BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
XX      anticonvulsant; ophthalmological; antidiabetic; virucide;
XX      antisense therapy; BAX antagonist; BAX inhibitor;
XX      familial amyotrophic lateral sclerosis; Alzheimer's disease;
XX      Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;

```

```

KW      diabetes-associated ocular disorder; scrapie infection;
KW      aberrant apoptosis; human; phosphorothioate; ss.
XX      Synthetic.
XX      Homo sapiens.
XX      Key Location/Qualifiers
XX      modified_base 1..20
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "phosphorothioate linkages, and all cytidine
XX      residues are 5-methylcytidines"
XX      modified_base 1..5
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      modified_base 16..20
XX      /tag= c
XX      /mod_base= OTHER
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XX      WO2003008543-A2.
XX      30-JAN-2003.
XX      13-JUL-2002; 2002WO-US022417.
XX      17-JUL-2001; 2001US-00908147.
XX      (ISIS-) ISIS PHARM INC.
XX      Zhang H, Watt AT;
XX      WPI; 2003-239321/23.
XX      New antisense compounds, useful for modulating the expression of BCL2-
XX      associated X (BAX) protein or for treating a disease or condition
XX      associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
XX      or Alzheimer's disease.
XX      Claim 3; Page 86; 139pp; English.
XX      The present invention describes a compound (I) 8-50 nucleobases in length
XX      targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
XX      protein, where the compound specifically hybridises with the nucleic acid
XX      molecule encoding BAX protein and inhibits the expression of BAX protein.
XX      The compound specifically hybridises with at least 8-nucleobase portion
XX      of an active site on a nucleic acid molecule encoding BAX protein. Also
XX      described: (1) a composition comprising (I) and a pharmaceutical carrier
XX      or diluent; (2) inhibiting the expression of BAX protein in cells or
XX      tissues comprising contacting the cells or tissues with (I); and (3)
XX      treating an animal having a disease or condition associated with BAX
XX      protein comprising administering to the animal (I) so that expression of
XX      BAX protein is inhibited. (I) has neurotropic, neuroprotective,
XX      antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
XX      virucide activities, and can be used in antisense therapy, and as a BAX
XX      antagonist. The antisense compounds (I) are useful for modulating the
XX      expression of BAX protein, and for treating a disease or condition
XX      associated with BAX protein, e.g. familial amyotrophic lateral
XX      sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
XX      cartilage-hair hyperplasia, diabetes-associated ocular disorders or
XX      scrapie infection, or a condition that arises from aberrant apoptosis.
XX      The compounds are useful as research reagents and in diagnostics. The
XX      present sequence represents a human BAX chimeric phosphorothioate
XX      oligonucleotide, which is used in an example from the present invention.
XX      Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX      Query Match 90.0%; Score 18; DB 8; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 2;
XX      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCCCAGTTGAAGTTCGCC 18

```

[illegible]

Query Match	85.0%;	Score 17;	DB 7;	Length 22;
Best Local Similarity	100.0%;	Pred. No. 7.5;		

CC The nucleotide sequence presented here is the target nucleic acid for
 CC nuclease-based cleavage reaction PG-RCA.
 XX
 SQ Sequence 24 BP; 5 A; 5 C; 6 G; 5 T; 3 U; 0 Other;
 Query Match 85.0%; Score 17; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CCAGTTGAAGTTGCCGT 20
 |||||
 Db 1 CCAGTTGAAGTTGCCGT 17
 |||||
 RESULT 5
 AEJ10484
 ID AEJ10484 standard; DNA; 24 BP.
 XX
 AC AEJ10484;
 XX
 DT 07-SEP-2006 (first entry)
 XX
 DE Target nucleic acid used in PG-RCA using ribbon probe.
 XX
 KW DNA detection; microorganism detection; SNP detection;
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;
 KW DNA methylation; gene amplification; primer extension; ss;
 KW DNA-RNA hybrid.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
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 FT /*tag= a
 FT modified_base 22..24
 FT /*tag= b
 FT /*mod_base= 2'-O-methyluridine
 XX
 PN WO2006074162-A2.
 XX
 PD 13-JUL-2006.
 XX
 PF 04-JAN-2006; 2006WO-US000086.
 XX
 PR 04-JAN-2005; 2005US-0641255P.
 PR 14-JUL-2005; 2005US-0699340P.
 XX
 XX (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 XX
 PI Murakami T;
 XX
 DR WPI; 2006-513365/52.
 XX
 PT Amplifying nucleic acid, by combining a nucleic acid primer with a
 PT polymerase and a circular nucleic acid probe, and producing a repeat of a
 PT sequence copy of the circular nucleic acid probe.
 XX
 PS Example 6; SEQ ID NO 16; 34pp; English.
 XX
 CC The present invention discloses a method of amplifying nucleic acid using
 CC primers and probes by rolling circle amplification method. The present
 CC invention comprises primer generation ? rolling circle amplification (PG-
 CC RCA) in which a ribbon probe is involved, allows the single step
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and
 CC rapidly. This technology is easily applicable to detection of other
 CC biomolecules such as DNA methylation, single nucleotide polymorphism
 CC (SNP), protein and posttranslational modifications. PCR (primer
 CC generation reaction) is a reaction that is designed to produce at least
 CC one nucleic acid primer from a PCR initiation sequence of an RCR (rolling
 CC circle reaction) product and the resulting primer is designed to prime to
 CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is
 CC designed to produce concatenated sequence copies of the circular probe,

CC in which the resulting product contains at least one PCR initiation
 CC sequence in every repeat sequence just like the initial reaction signal.
 CC The first and second nucleic acid primers are generated by one of
 CC nuclease-based cleavage reaction, strand displacement amplification,
 CC cleavage-initiated isothermal amplification, three-way junction
 CC isothermal amplification, three-way junction rolling circle reaction,
 CC binding assay using a nucleic acid labeled recognition agent and
 CC proximity assay. The method of nucleic acid detection using the present
 CC invention is useful for in vitro diagnostics and in pathogen detection.
 CC The nucleotide sequence presented here is the target nucleic acid used in
 CC PG-RCA using ribbon probe.
 XX
 SQ Sequence 24 BP; 5 A; 5 C; 6 G; 5 T; 3 U; 0 Other;
 Query Match 85.0%; Score 17; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CCAGTTGAAGTTGCCGT 20
 |||||
 Db 1 CCAGTTGAAGTTGCCGT 17
 |||||
 RESULT 6
 AEJ10483/C
 ID AEJ10483 standard; DNA; 42 BP.
 XX
 AC AEJ10483;
 XX
 DT 07-SEP-2006 (first entry)
 XX
 DE Circularizable lock probe used for ribbon probe synthesis.
 XX
 KW DNA detection; microorganism detection; SNP detection;
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;
 KW DNA methylation; gene amplification; primer extension; probe; PCR;
 KW circular; ss; DNA-RNA hybrid.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 16..19
 FT /*tag= a
 XX
 PN WO2006074162-A2.
 XX
 PD 13-JUL-2006.
 XX
 PF 04-JAN-2006; 2006WO-US000086.
 XX
 PR 04-JAN-2005; 2005US-0641255P.
 PR 14-JUL-2005; 2005US-0699340P.
 XX
 XX (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 XX
 PI Murakami T;
 XX
 DR WPI; 2006-513365/52.
 XX
 PT Amplifying nucleic acid, by combining a nucleic acid primer with a
 PT polymerase and a circular nucleic acid probe, and producing a repeat of a
 PT sequence copy of the circular nucleic acid probe.
 XX
 PS Example 5; SEQ ID NO 15; 34pp; English.
 XX
 CC The present invention discloses a method of amplifying nucleic acid using
 CC primers and probes by rolling circle amplification method. The present
 CC invention comprises primer generation ? rolling circle amplification (PG-
 CC RCA) in which a ribbon probe is involved, allows the single step
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and
 CC rapidly. This technology is easily applicable to detection of other
 CC biomolecules such as DNA methylation, single nucleotide polymorphism

CC (SNP), protein and posttranslational modifications. PCR (primer
 CC generation reaction) is a reaction that is designed to produce at least
 CC one nucleic acid primer from a PCR initiation sequence of an RCR (rolling
 CC circle reaction) product and the resulting primer is designed to prime to
 CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is
 CC designed to produce concatenated sequence copies of the circular probe,
 CC in which the resulting product contains at least one PCR initiation
 CC sequence in every repeat sequence just like the initial reaction signal.
 CC The first and second nucleic acid primers are generated by one of
 CC nuclease-based cleavage reaction, strand displacement amplification,
 CC cleavage-initiated isothermal amplification, three-way junction
 CC isothermal amplification, three-way junction rolling circle reaction,
 CC binding assay using a nucleic acid labeled recognition agent and
 CC proximity assay. The method of nucleic acid detection using the present
 CC invention is useful for in vitro diagnostics and in pathogen detection.
 CC The nucleotide sequence presented here is the circularizable lock probe
 CC used for ribbon probe synthesis.

XX Sequence 42 BP; 12 A; 10 C; 12 G; 7 T; 1 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20
 |||||
 Db 35 CCAGTTGAAGTTGCCGT 19

RESULT 7

AEJ10476/c
 ID AEJ10476 standard; DNA; 44 BP.

AC AEJ10476;

DT 07-SEP-2006 (first entry)

XX Circularizable probe for nuclease-based cleavage reaction PG-RCA.

DE DNA detection; microorganism detection; SNP detection;
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;
 KW DNA methylation; gene amplification; primer extension; probe; PCR;
 KW circular; ss.

OS Synthetic.

PN WO2006074162-A2.

PD 13-JUL-2006.

PF 04-JAN-2006; 2006WO-US000086.

PR 04-JAN-2005; 2005US-0641255P.

PR 14-JUL-2005; 2005US-0699340P.

XX (HITB) HITACHI CHEM CO LTD.

PA (HITB) HITACHI CHEM RES CENT INC.

PI Murakami T;

XX WPI; 2006-513365/52.

XX Amplifying nucleic acid, by combining a nucleic acid primer with a
 PT polymerase and a circular nucleic acid probe, and producing a repeat of a
 PT sequence copy of the circular nucleic acid probe.

XX Example 3; SEQ ID NO 8; 34pp; English.

XX The present invention discloses a method of amplifying nucleic acid using
 CC primers and probes by rolling circle amplification method. The present
 CC invention comprises primer generation ? rolling circle amplification (PG-
 CC RCA) in which a ribbon probe is involved, allows the single step
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and

CC rapidly. This technology is easily applicable to detection of other
 CC biomolecules such as DNA methylation, single nucleotide polymorphism
 CC (SNP), protein and posttranslational modifications. PGR (primer
 CC generation reaction) is a reaction that is designed to produce at least
 CC one nucleic acid primer from a PGR initiation sequence of an RCR (rolling
 CC circle reaction) product and the resulting primer is designed to prime to
 CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is
 CC designed to produce concatenated sequence copies of the circular probe,
 CC in which the resulting product contains at least one PCR initiation
 CC sequence in every repeat sequence just like the initial reaction signal.
 CC The first and second nucleic acid primers are generated by one of
 CC nuclease-based cleavage reaction, strand displacement amplification,
 CC cleavage-initiated isothermal amplification, three-way junction
 CC isothermal amplification, three-way junction rolling circle reaction,
 CC binding assay using a nucleic acid labeled recognition agent and
 CC proximity assay. The method of nucleic acid detection using the present
 CC invention is useful for in vitro diagnostics and in pathogen detection.
 CC The nucleotide sequence presented here is the circularizable probe for
 CC nuclease-based cleavage reaction PG-RCA.

SQ Sequence 44 BP; 10 A; 13 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 44;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20

|||||

Db 28 CCAGTTGAAGTTGCCGT 12

RESULT 8

AEJ10482/c

ID AEJ10482 standard; DNA; 44 BP.

AC AEJ10482;

DT 07-SEP-2006 (first entry)

XX Circularizable probe used for ribbon probe synthesis.

DE DNA detection; microorganism detection; SNP detection;
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;
 KW DNA methylation; gene amplification; primer extension; probe; PCR;
 KW circular; ss.

OS Synthetic.

PN WO2006074162-A2.

PD 13-JUL-2006.

PF 04-JAN-2006; 2006WO-US000086.

PR 04-JAN-2005; 2005US-0641255P.

PR 14-JUL-2005; 2005US-0699340P.

XX (HITB) HITACHI CHEM CO LTD.

PA (HITB) HITACHI CHEM RES CENT INC.

PI Murakami T;

XX WPI; 2006-513365/52.

XX Amplifying nucleic acid, by combining a nucleic acid primer with a
 PT polymerase and a circular nucleic acid probe, and producing a repeat of a
 PT sequence copy of the circular nucleic acid probe.

XX Example 5; SEQ ID NO 14; 34pp; English.

XX The present invention discloses a method of amplifying nucleic acid using
 CC primers and probes by rolling circle amplification method. The present
 CC invention comprises primer generation ? rolling circle amplification (PG-
 CC RCA) in which a ribbon probe is involved, allows the single step
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and

CC RCA) in which a ribbon probe is involved, allows the single step
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and
 CC rapidly. This technology is easily applicable to detection of other
 CC biomolecules such as DNA methylation, single nucleotide polymorphism
 CC (SNP), protein and posttranslational modifications. PCR (primer
 CC generation reaction) is a reaction that is designed to produce at least
 CC one nucleic acid primer from a PCR initiation sequence of an RCR (rolling
 CC circle reaction) product and the resulting primer is designed to prime to
 CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is
 CC designed to produce concatenated sequence copies of the circular probe,
 CC in which the resulting product contains at least one PCR initiation
 CC sequence in every repeat sequence just like the initial reaction signal.
 CC The first and second nucleic acid primers are generated by one of
 CC nuclease-based cleavage reaction, strand displacement amplification,
 CC isothermal-initiated isothermal amplification, three-way junction
 CC cleavage-initiated isothermal amplification, rolling circle reaction,
 CC binding assay using a nucleic acid labeled recognition agent and
 CC proximity assay. The method of nucleic acid detection using the present
 CC invention is useful for in vitro diagnostics and in pathogen detection.
 CC The nucleotide sequence presented here is the circularizable probe used
 CC for ribbon probe synthesis.

XX SQ Sequence 44 BP; 10 A; 13 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 44;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20

Db 28 CCAGTTGAAGTTGCCGT 12

RESULT 9

AEJ10475/C
 ID AEJ10475 standard; DNA; 45 BP.

AC AEJ10475;

XX 07-SEP-2005 (first entry)

XX PGR probe for nuclease-based cleavage reaction PG-RCA.

XX DNA detection; microorganism detection; SNP detection;
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;
 KW DNA methylation; gene amplification; primer extension; probe; PCR;
 KW primer; DNA-RNA hybrid; ss.

XX Synthetic.

XX Key Location/Qualifiers

EH misc_RNA 23..26

ET /*tag= a

FT misc_RNA 43..45

FT /*tag= b

ET modified_base 43..45

ET /*tag= c

ET /*mod_base= 2'-O-methyluridine

XX WO2006074162-A2.

XX 13-JUL-2006.

XX 04-JAN-2005; 2006WO-US000086.

XX 04-JAN-2005; 2005US-0641255P.

XX 14-JUL-2005; 2005US-0699340P.

XX (HITB) HITACHI CHEM CO LTD.

EA (HITB) HITACHI CHEM RES CENT INC.

XX Murakami T;

XX

DR WPI; 2006-513365/52.

XX Amplifying nucleic acid, by combining a nucleic acid primer with a
 PT polymerase and a circular nucleic acid probe, and producing a repeat of a
 PT sequence copy of the circular nucleic acid probe.

XX Example 3; SEQ ID NO 7; 34pp; English.

XX The present invention discloses a method of amplifying nucleic acid using
 CC primers and probes by rolling circle amplification method. The present
 CC invention comprises primer generation ? rolling circle amplification (PG-
 CC RCA) in which a ribbon probe is involved, allows the single step
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and
 CC rapidly. This technology is easily applicable to detection of other
 CC biomolecules such as DNA methylation, single nucleotide polymorphism
 CC (SNP), protein and posttranslational modifications. PCR (primer
 CC generation reaction) is a reaction that is designed to produce at least
 CC one nucleic acid primer from a PCR initiation sequence of an RCR (rolling
 CC circle reaction) product and the resulting primer is designed to prime to
 CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is
 CC designed to produce concatenated sequence copies of the circular probe,
 CC in which the resulting product contains at least one PCR initiation
 CC sequence in every repeat sequence just like the initial reaction signal.
 CC The first and second nucleic acid primers are generated by one of
 CC nuclease-based cleavage reaction, strand displacement amplification,
 CC cleavage-initiated isothermal amplification, three-way junction
 CC isothermal amplification, three-way junction rolling circle reaction,
 CC binding assay using a nucleic acid labeled recognition agent and
 CC proximity assay. The method of nucleic acid detection using the present
 CC invention is useful for in vitro diagnostics and in pathogen detection.
 CC The nucleotide sequence presented here is the PGR probe for nuclease-
 CC based cleavage reaction PG-RCA.

XX SQ Sequence 45 BP; 12 A; 10 C; 12 G; 7 T; 4 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 45;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20

Db 42 CCAGTTGAAGTTGCCGT 26

RESULT 10

ABX13068

ID ABX13068 standard; DNA; 20 BP.

XX AC ABX13068;

XX 29-MAY-2003 (first entry)

XX Human bax PCR primer #2.

XX Human; insulin-like growth factor binding protein 5; IGFBP-5; primer; ss;
 KW cytostatic; apoptosis; cancer; breast; prostate; ovary; lung; colon; PCR;
 KW bax.

XX Homo sapiens.

XX WO2003006029-A1.

XX 23-JAN-2003.

XX 15-JUL-2002; 2002WO-AU000936.

XX 13-JUL-2001; 2001AU-00006331.

XX (UNSY) UNIV SYDNEY.

XX Baxter RC, Butt AJ;

XX WPI; 2003-221646/21.

DR

XX Inducing apoptosis in cancer cell, useful for treating cancer, e.g.
PT breast or prostate cancer comprises increasing the expression of insulin-
PT like growth factor binding protein-5 (IGFBP-5) by the cell to an
PT apoptosis-inducing amount.
XX
XX Example; Page 29; 65pp; English.
XX
CC The invention relates to a method for inducing apoptosis in a cancer cell
CC comprising increasing the expression of insulin-like growth factor
CC binding protein 5 (IGFBP-5) by the cell to an apoptosis-inducing amount.
CC The invention also relates to a method of sensitising a cancer cell to
CC stimuli that induce apoptosis by increasing the expression of IGFBP-5 by
CC the cell, a method of killing a cancer cell by sensitising the cell to
CC stimuli that induce apoptosis and simultaneously exposing the cell to
CC apoptosis-inducing stimuli, or exposing the cell to apoptosis-inducing
CC stimuli and simultaneously or subsequently increasing the expression of
CC IGFBP-5 by the cell to an apoptosis-inducing amount. The methods are
CC useful for treating cancer, such as breast, prostate, ovarian, lung or
CC colon cancer, by inducing apoptosis or killing cancer cells. This
CC sequence represents a bax PCR primer used in the method of the invention
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CAGTTGAAGTTCGGT 20
|||||
Db 1 CAGTTGAAGTTCGGT 16
RESULT 11
ADA20946
ID ADA20946 standard; DNA; 20 BP.
XX
AC ADA20946;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mouse BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:119.
XX
KW BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; ophthalmological; antidiabetic; virucide;
KW antisense therapy; BAX antagonist; BAX inhibitor;
KW familial amyotrophic lateral sclerosis; Alzheimer's disease;
KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;
KW diabetes-associated ocular disorder; scrapie infection;
KW aberrant apoptosis; mouse; phosphorothioate; ss.
XX
OS Synthetic.
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages, and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2003008543-A2.
XX
XX 30-JAN-2003.
XX

PF 13-JUL-2002; 2002WO-US022417.
XX
PR 17-JUL-2001; 2001US-00908147.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX WPI; 2003-239321/23.
XX
XX New antisense compounds, useful for modulating the expression of BCL2-
PT associated X (BAX) protein or for treating a disease or condition
PT associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
PT or Alzheimer's disease.
XX
PS Claim 3; Page 93; 139pp; English.
XX
CC The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
CC protein, where the compound specifically hybridises with the nucleic acid
CC molecule encoding BAX protein and inhibits the expression of BAX protein.
CC The compound specifically hybridises with at least 8-nucleobase portion
CC of an active site on a nucleic acid molecule encoding BAX protein. Also
CC described: (1) a composition comprising (I) and a pharmaceutical carrier
CC or diluent; (2) inhibiting the expression of BAX protein in cells or
CC tissues comprising contacting the cells or tissues with (I); and (3)
CC treating an animal having a disease or condition associated with BAX
CC protein comprising administering to the animal (I) so that expression of
CC BAX protein is inhibited. (I) has neurotropic, neuroprotective,
CC antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
CC virucide activities, and can be used in antisense therapy, and as a BAX
CC antagonist. The antisense compounds (I) are useful for modulating the
CC expression of BAX protein, and for treating a disease or condition
CC associated with BAX protein, e.g. familial amyotrophic lateral
CC sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
CC cartilage-hair hyperplasia, diabetes-associated ocular disorders or
CC scrapie infection, or a condition that arises from aberrant apoptosis.
CC The compounds are useful as research reagents and in diagnostics. The
CC present sequence represents a mouse BAX chimeric phosphorothioate
CC oligonucleotide, which is used in an example from the present invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCCAGTTGAAGTTCGC 18
|||||
Db 1 CCCAGTTGAAGTTCGC 16
RESULT 12
AED12216
ID AED12216 standard; DNA; 20 BP.
XX
AC AED12216;
XX
DT 01-DEC-2005 (first entry)
XX
DE Bax (human) RT-PCR primer SEQ ID 16.
XX
KW Drug screening; apoptosis; protein interaction; Bax; Cytostatic;
KW Neuroprotective; cancer; neurodegenerative disease; ss; RT-PCR;
KW reverse transcriptase PCR; primer.
XX
OS Homo sapiens.
XX
XX WO2005093082-A1.
XX
XX 06-OCT-2005.
XX
XX 23-MAR-2005; 2005WO-JP005247.
XX

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XX 26-MAR-2004; 2004JP-00093266.
PR 14-JUN-2004; 2004JP-00176107.
XX
XX (HISM ) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
XX Nakagawara A, Ozaki T;
XX WPI; 2005-713863/73.
XX
XX Screening compound capable of stimulating or inhibiting apoptosis,
PT involves judging compound capable of intensifying interaction between p73
PT and IKK-alpha as compound capable of stimulating or inhibiting apoptosis.
XX
XX Example; SEQ ID NO 16; 79pp; Japanese.
XX
XX The invention relates to screening (MI) a compound capable of stimulating
CC or inhibiting apoptosis, comprising identifying a compound capable of
CC modulating the interaction between p73 and IKK-alpha (IkappaB kinase) as
CC a compound capable of stimulating or inhibiting apoptosis. The method
CC comprise culturing a cell that expresses p73 and IKK-alpha in the
CC presence or absence of test compound, measuring an interaction between
CC p73 and IKK-alpha in each cultured cell and judging a compound as being
CC capable of stimulating or inhibiting apoptosis, when an interaction
CC between p73 and IKK-alpha in the cell cultured in the presence of test
CC compound, is stronger or weaker, in comparison to cell cultured in the
CC absence of test compound, respectively. Also included are an apoptosis
CC stimulator comprising AED12224 (human IKK-alpha, or a nucleic acid that
CC encodes human IKK-alpha) and an apoptosis inhibitor comprising human IKK-
CC alpha K44A mutant (AED12225) or human ubiquitin fusion degradation
CC protein-2a (AED12226). The method is useful for screening a compound
CC capable of stimulating or inhibiting apoptosis utilized for treating
CC cancer or neurodegenerative diseases. The present sequence is an RT-PCR
CC primer for a non-IKK mRNA (i.e. is either a control or is for an IKK
CC binding protein).
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 16; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CAGTTGAAGTTGCCGT 20
DB 1 CAGTTGAAGTTGCCGT 16
RESULT 13
AEJ97326
ID AEJ97326 standard; DNA; 20 BP.
AC AEJ97326;
XX
XX 02-NOV-2006 (first entry)
DT
DE RT-PCR primer BAX reverse, SEQ ID 8.
XX
XX Therapeutic; apoptosis inhibition; apoptosis stimulation; neoplasm;
KW cancer; neurodegenerative disease; neurological disorder; RT-PCR; primer;
KW ss.
XX
XX Homo sapiens.
OS
XX JP2006223265-A.
PN
XX 31-AUG-2006.
PD
XX 21-FEB-2005; 2005JP-00044554.
PF
XX 21-FEB-2005; 2005JP-00044554.
PR
XX (HISM ) HISAMITSU PHARM CO LTD.
PA

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PA (CHIB-) CHIBA PREFECTURE.
XX
XX Nakagawara A, Ozaki T;
XX WPI; 2006-590511/61.
XX
XX Screening compound capable of promoting or suppressing apoptosis, for
PT treating cancer or neurodegenerative disease, involves determining
PT whether compound inhibits or enhances interaction of p53 and NFBD1.
XX
XX Example; SEQ ID NO 8; 21pp; Japanese.
XX
XX The invention relates to the screening of a compound capable of promoting
CC or suppressing apoptosis. The method comprises determining whether a
CC compound inhibits or enhances the interaction of p53 and NFBD1 (nuclear
CC factor with BRCT domains protein 1), or culturing a cell expressing p53
CC and NFBD1 in the presence and in the absence of a test compound and
CC measuring the interaction of p53 and NFBD1 in a cultured cell. Further,
CC disclosed is an apoptosis inhibitor with p53 binding activity having an
CC amino acid sequence as given in AEJ97331. The method is useful for
CC screening a compound that promotes or suppresses apoptosis and is useful
CC as a therapeutic agent for cancer and neurodegenerative disorders. The
CC current sequence represents an RT-PCR primer used in an exemplification
CC of the invention.
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 16; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CAGTTGAAGTTGCCGT 20
DB 1 CAGTTGAAGTTGCCGT 16
RESULT 14
AEK58344
ID AEK58344 standard; DNA; 20 BP.
XX
XX AEK58344;
AC
XX
XX 16-NOV-2006 (first entry)
DT
DE Interferon-related gene specific PCR primer, SEQ ID NO:21.
XX
XX screening; gene expression; hepatitis C virus infection;
KW antiinflammatory; hepatotropic; virucide; gastrointestinal disease;
KW infection; diagnostic; diagnosis; liver cirrhosis; inflammation;
KW microarray; DNA amplification; therapeutic; ss; primer; PCR; interferon.
XX
XX Homo sapiens.
OS
XX WO2006085407-A1.
PN
XX 17-AUG-2006.
PD
XX 30-SEP-2005; 2005WO-JP018573.
PF
XX 09-FEB-2005; 2005JP-00033707.
PR
XX (UYNI-) UNIV NIPPON.
PA
XX Esami M, Takayama T;
XX WPI; 2006-680124/70.
XX
XX Screening gene whose expression is increased in high/low hepatitis C
PT virus (HCV) tissue, involves selecting gene based on its expression level
PT in low and high virus group tissues being selected based on HCV 18S rRNA
PT analysis.
XX
XX Example 1; SEQ ID NO 21; 75pp; Japanese.
PS

```

XX The new invention relates to screening a gene whose expression is
CC increased in high hepatitis C virus (HCV) group tissue or low HCV group
CC tissue. The method involves selecting liver tissue whose value is
CC obtained by dividing copy number of HCV per 50 ng of liver tissue-derived
CC cDNA by the value of 18S rRNA is not more than 300 units as low virus
CC group tissue and not more than 3000 units as high virus group tissue,
CC measuring gene expression level in tissues, and selecting gene whose
CC expression is increased in high/low virus group tissue more than low/high
CC virus group tissue. Also described is a diagnostic of diseases relevant
CC to viral load, comprising (a) gene (e.g. OASL, EHF, CXCL6, IRS2, MAP1B
CC and CXCL10) with a sequence of one of SEQ ID No. 54-131, where the
CC expression of the gene enhances in high virus group, (b) gene (e.g.
CC FLJ4615, 28S rRNA, ENCL, RAP1, BAGE and PSMA8) comprising a sequence of
CC one of SEQ ID No. 132-170, where the expression of the gene enhances in
CC low virus group, (c) one of gene (e.g. HLA-DQA1, TMPSR52, SPEC2, SNA12,
CC IFI44, LEPK and FNB1) of CHH gene cluster comprising a sequence of SEQ
CC ID No. 171-237, where the expression of the gene enhances in high virus
CC group of chronic hepatitis, (d) one of gene (e.g. FLJ46154, KCNN2, CRP,
CC LOC134145 and HMG2) of CHL gene cluster comprising a sequence of SEQ ID
CC No. 238-258, where the expression of the gene enhances in low virus group
CC of chronic hepatitis, (e) one of gene (e.g. SDS, GLP2, KLF6, ZDHHC11,
CC GADD45D, MX1 and BCU3) of LCH gene cluster comprising a sequence of one
CC of SEQ ID No. 259-285, where the expression of the gene enhances in high
CC virus group of liver cirrhosis, or (f) one of gene (e.g. MND4, CLECSF12,
CC SUC8A1, PST, API52, LARS and TBC1D1) of LCL gene cluster comprising a
CC sequence of one of SEQ ID No. 286-302, where the expression of the gene
CC enhances in low virus group of liver cirrhosis. The measurement of
CC expression is carried out using microarray and/or real-time PCR. The
CC method is useful for screening a gene whose expression is increased in a
CC high virus group tissue containing a large amount of HCV or in a low
CC virus group tissue containing small amount of HCV, for development of
CC therapeutic agent of HCV. This sequence is a primer for PCR amplification
CC of an interferon-related gene, useful in the new method of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
Db 1 CAGTTGAAGTTGCCGT 16

RESULT 15

AEH24548/c
ID AEH24548 standard; DNA; 22 BP.

AC AEH24548;

XX 29-JUN-2006 (first entry)

XX BAX gene forward PCR primer.

XX ss; PCR; primer; drug metabolism; cancer; cytostatic; neoplasm;
KW immune inhibition; apoptosis stimulation; RNA quantitation; BAX.

XX Homo sapiens.

XX WO2006045053-A2.

XX 27-APR-2006.

XX 20-OCT-2005; 2005WO-US037925.

XX 20-OCT-2004; 2004US-0620603P.

XX 16-FEB-2005; 2005US-0653557P.

XX 08-JUN-2005; 2005US-0688741P.

XX (HITB) HITACHI CHEM CO LTD.

PA (HITB) HITACHI CHEM RES CENT INC.

XX Mitsuhaashi M;
PI
XX
DR WPI; 2006-332057/34.

XX Measuring a patient's responsiveness to a drug comprises exposing whole
PT blood of the patient to the drug for 7 hours or less, and measuring the
PT amount of an mRNA associated with an effect of the drug in blood cells.

XX Disclosure; SEQ ID NO 39; 74pp; English.

XX The invention relates to a method of measuring a patient's responsiveness
CC to a which drug comprises exposing whole blood of the patient to the drug
CC for 7 hours or less, and measuring the amount of an mRNA associated with
CC an effect of the drug in blood cells. Preferably, the amount of the mRNA
CC present in the blood cells is measured before the exposure, and the
CC change in the amount of the mRNA is determined by comparing the amount of
CC mRNA measured before exposure to the amount of mRNA measured after
CC exposure. The method additionally comprises exposing whole blood of the
CC patient to a control vehicle for 7 hours or less; after the exposure,
CC measuring the amount of the mRNA associated with an effect of the drug in
CC the blood cells exposed to the control vehicle; and identifying
CC responsiveness to the drug includes comparing results of the measurement
CC obtained after exposure to the control vehicle with results of the
CC measurement obtained after exposure to the drug. The control vehicle is
CC selected from phosphate-buffered saline and dimethyl sulfoxide. The mRNA
CC is selected from mRNAs encoding the gene products of the Bcl-2/Bax gene
CC family, Bax gene product, the BH3-only Bcl-2 gene family, ATP-binding
CC cassette subfamilies A to G, and p21, PUMA and NOXA gene products. The
CC method is useful for measuring a patient's responsiveness to a drug,
CC which is useful in developing an optimized treatment protocol tailored to
CC the specific patient. The method may be used for patients with conditions
CC such as cancer or diseases which require immunosuppression. The present
CC sequence represents BAX gene forward PCR primer. This gene was amplified
CC in studies of drug induced apoptosis in tailored drug administration for
CC leukemia and lymphoma.

XX Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 22;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

Search completed: December 3, 2007, 16:22:19
Job time : 1240 secs

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:58:53 ; Search time 221 Seconds
(without alignments)
339.009 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagttgaagttgcgct 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 187302446 residues

Total number of hits satisfying chosen parameters: 43

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum Score over Length 70%

Listing first 1000 summaries

Database : Issued Patents NA:*

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- 2: /EMC_Celerra_SIDS2/ptodata/1/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A COMB.seq:*
- 6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B COMB.seq:*
- 7: /EMC_Celerra_SIDS2/ptodata/1/ina/H COMB.seq:*
- 8: /EMC_Celerra_SIDS2/ptodata/1/ina/PTUS COMB.seq:*
- 9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP COMB.seq:*
- 10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE COMB.seq:*
- 11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.4	81.4	57.0	14	US-09-341-700A-857
C 2	12	80.0	60.0	15	US-08-584-040-8471
C 3	12	80.0	60.0	15	US-09-371-772B-4126
C 4	12	80.0	60.0	15	US-09-685-664B-4126
C 5	12	80.0	60.0	15	US-10-138-674B-4126
C 6	10.4	74.3	52.0	14	US-09-168-791-14
C 7	10.4	74.3	52.0	14	US-09-168-714-14
C 8	11.8	73.8	59.0	16	US-09-371-772B-5807
C 9	11.8	73.8	59.0	16	US-10-138-674B-5807
C 10	11	73.3	55.0	15	US-08-584-040-8496
C 11	11	73.3	55.0	15	US-09-371-772B-4150
C 12	11	73.3	55.0	15	US-09-685-664B-4150
C 13	11	73.3	55.0	15	US-10-138-674B-4150
C 14	8.8	73.3	44.0	12	US-08-441-887A-238
C 15	8.8	73.3	44.0	12	US-08-441-887A-239
C 16	8.8	73.3	44.0	12	US-09-417-455-22
C 17	8.8	73.3	44.0	12	US-09-348-942-22
C 18	8.8	73.3	44.0	12	US-09-457-626-22
C 19	8.8	73.3	44.0	12	US-09-576-008-22
C 20	8.8	73.3	44.0	12	US-08-510-521E-357
C 21	8.8	73.3	44.0	12	US-08-510-521E-358
C 22	8.8	73.3	44.0	12	US-10-070-588A-32
C 23	13.8	72.6	69.0	19	US-10-310-914B-801404

C 24	10	71.4	50.0	14	US-09-341-700A-858	Sequence 8
C 25	12.8	71.1	64.0	18	US-10-310-914B-1258144	Sequence 1
C 26	12	70.6	60.0	17	US-08-584-040-3879	Sequence 3
C 27	12	70.6	60.0	17	US-08-584-040-3880	Sequence 3
C 28	12	70.6	60.0	17	US-09-371-772B-1646	Sequence 1
C 29	12	70.6	60.0	17	US-09-371-772B-1647	Sequence 1
C 30	12	70.6	60.0	17	US-09-371-772B-6253	Sequence 6
C 31	12	70.6	60.0	17	US-09-371-772B-6254	Sequence 6
C 32	12	70.6	60.0	17	US-09-685-664B-1646	Sequence 1
C 33	12	70.6	60.0	17	US-09-685-664B-1647	Sequence 1
C 34	12	70.6	60.0	17	US-10-138-674B-1646	Sequence 1
C 35	12	70.6	60.0	17	US-10-138-674B-1647	Sequence 1
C 36	12	70.6	60.0	17	US-10-138-674B-6253	Sequence 6
C 37	12	70.6	60.0	17	US-10-138-674B-6254	Sequence 6
C 38	12	70.6	60.0	17	US-10-138-674B-8571	Sequence 8
C 39	13.4	70.5	67.0	19	US-10-310-914B-1191074	Sequence 1
C 40	8.4	70.0	42.0	12	US-08-401-512-16	Sequence 1
C 41	8.4	70.0	42.0	12	US-08-738-381-48	Sequence 4
C 42	8.4	70.0	42.0	12	US-10-078-958-50	Sequence 5
C 43	8.4	70.0	42.0	12	US-10-078-958-59	Sequence 5

ALIGNMENTS

RESULT 1
US-09-341-700A-857
; Sequence 857, Application US/09341700A
; Patent No. 6972171
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/09/341,700A
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 857
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-09-341-700A-857

Query Match 57.0%; Score 11.4; DB 4; Length 14;
Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 5.4e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
|||||||
Db 2 GTTGAAGTTGCTG 14

RESULT 2
US-08-584-040-8471/c
; Sequence 8471, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ STATE: Los Angeles
/ COUNTRY: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 8471:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-8471

Query Match 60.0%; Score 12; DB 3; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 3

US-09-371-772B-4126/c
/ Sequence 4126, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00.876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4126
/ LENGTH: 15

/ TYPE: RNA
/ ORGANISM: Mus sp.
/ US-09-371-772B-4126

Query Match 60.0%; Score 12; DB 3; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 4

US-09-685-664B-4126/c
/ Sequence 4126, Application US/09685664B
/ Patent No. 6818447
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-K (400/021)
/ CURRENT APPLICATION NUMBER: US/09/685,664B
/ CURRENT FILING DATE: 2000-10-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ PRIOR APPLICATION NUMBER: US 09/371,772
/ PRIOR FILING DATE: 1999-08-10
/ NUMBER OF SEQ ID NOS: 8231
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4126
/ LENGTH: 15
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-09-685-664B-4126

Query Match 60.0%; Score 12; DB 3; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 5

US-10-138-674B-4126/c
/ Sequence 4126, Application US/10138674B
/ Patent No. 7034009
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/138,674B
/ CURRENT FILING DATE: 2002-05-03
/ NUMBER OF SEQ ID NOS: 20829
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4126
/ LENGTH: 15
/ TYPE: RNA

Db 2 GACCCAGAGAAGUU 16

RESULT 10

US-08-584-040-8496/c
; Sequence 8496, Application US/08584040

; Patent No. 6346398

; GENERAL INFORMATION:

; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: TREATMENT OF DISEASES OR

; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

; TITLE OF INVENTION: GROWTH FACTOR

; NUMBER OF SEQUENCES: 8502

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: Storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/584,040

; FILING DATE: January 11, 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/005,974

; FILING DATE: October 26, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 218/064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 8496:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-584-040-8496

Query Match 55.0%; Score 11; DB 3; Length 15;

Score over Length 73.3%;

Best Local Similarity 100.0%; Pred. No. 8.5e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14

Db 15 CCAGTTGAAGT 5

RESULT 11

US-09-371-772B-4150/c

; Sequence 4150, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-4150

Query Match 55.0%; Score 11; DB 3; Length 15;

Score over Length 73.3%;

Best Local Similarity 100.0%; Pred. No. 8.5e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14

Db 15 CCAGTTGAAGT 5

RESULT 12

US-09-685-664B-4150/c

; Sequence 4150, Application US/09685664B

; Patent No. 6818447

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBH00-876-K (400/021)

; CURRENT APPLICATION NUMBER: US/09/685,664B

; CURRENT FILING DATE: 2000-10-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; PRIOR APPLICATION NUMBER: US 09/371,772

; PRIOR FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 8231

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4150

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-685-664B-4150

Query Match 55.0%; Score 11; DB 3; Length 15;

Score over Length 73.3%;

Best Local Similarity 100.0%; Pred. No. 8.5e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14

Db 15 CCAGTTGAAGT 5

RESULT 13

US-10-138-674B-4150/c

; Sequence 4150, Application US/10138674B

; Patent No. 7034009

; GENERAL INFORMATION:

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-239

Query Match 44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
|||||
Db 1 ATTGGAGTTGC 12

RESULT 16

US-09-417-455-22
; Sequence 22, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Exon
US-09-417-455-22

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13
|||||
Db 1 CCACAGGTGAAG 12

RESULT 17

US-09-348-942-22
; Sequence 22, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07

; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Exon
US-09-348-942-22

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13
|||||
Db 1 CCACAGGTGAAG 12

RESULT 18

US-09-457-626-22
; Sequence 22, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US/09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12

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; TYPE: DNA
; ORGANISM: Exon
US-09-457-626-22

Query Match      44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
   |||||
Db 1 CCACAGGTGAAG 12

RESULT 19
US-09-576-008-22
; Sequence 22, Application US/09576008
; Patent No. 6541623
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-Yue
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US/09/576,008
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: - US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Exon
US-09-576-008-22

Query Match      44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
   |||||
Db 1 CCACAGGTGAAG 12

RESULT 20
US-08-510-521E-357
; Sequence 357, Application US/08510521E
```

```
; Patent No. 7115364
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; Cronin, Maureen T.
; Fodor, Stephen P.A.
; Gingeras, Thomas R.
; Huang, Xiaohua C.
; Hubbell, Earl A.
; Lipshutz, Robert J.
; Lobban, Peter E.
; Morris, Macdonald S.
; Garrett Miyada, Charles
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; NUMBER OF SEQUENCES: 585
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: 2 Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/510,521E
; FILING DATE: 02-Aug-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 357:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; SEQUENCE DESCRIPTION: SEQ ID NO: 357:
US-08-510-521E-357

Query Match      44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
   |||||
Db 1 TGGAGTTGCAGT 12

RESULT 21
US-08-510-521E-358
; Sequence 358, Application US/08510521E
; Patent No. 7115364
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; Cronin, Maureen T.
; Fodor, Stephen P.A.
```

; Gingeras, Thomas R.
; Huang, Xiaohua C.
; Hubbell, Earl A.
; Lipshutz, Robert J.
; Lobban, Peter E.
; Garrett Miyada, Charles
; Morris, Macdonald S.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; Biological Chips
; NUMBER OF SEQUENCES: 585
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: 2 Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/510,521E
; FILING DATE: 02-Aug-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; SEQUENCE DESCRIPTION: SEQ ID NO: 358:
US-08-510-521E-358

Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 1 ATTGGAGTTGC 12

RESULT 22
US-10-070-588A-32
; Sequence 32, Application US/10070588A
; Patent No. 7122652
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS AG
; TITLE OF INVENTION: Polymorphisms in the human hpxr gene and their use in
; diagnostic and therapeutic applications
; FILE REFERENCE: D 2145 PCT-2
; CURRENT APPLICATION NUMBER: US/10/070,588A
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: PCT/EP00/08827
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: variant of human pregnane X
; OTHER INFORMATION: receptor (hpxr) gene
US-10-070-588A-32

Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13
Db 1 CCCAGGTGAGG 12

RESULT 23
US-10-310-914B-801404/C
; Sequence 801404, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 801404
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-801404

Query Match 69.0%; Score 13.8; DB 6; Length 19;
Score over Length 72.6%;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGCC 18
Db 17 CCACATTTGAAGTTGCC 1

RESULT 24
US-09-341-700A-858
; Sequence 858, Application US/09341700A
; Patent No. 6972171
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/09/341,700A
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 858
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-09-341-700A-858

Query Match      50.0%; Score 10; DB 4; Length 14;
Score over Length 71.4%;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
   |||||
Db 5 GTTGAAGTTG 14

RESULT 25
US-10-310-914B-1258144/c
; Sequence 1258144, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1258144
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1258144

Query Match      64.0%; Score 12.8; DB 6; Length 18;
Score over Length 71.1%;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCCT 20
   |||||
Db 17 CAGTTGAAGTTGCACT 2

RESULT 26
US-08-584-040-3879/c
; Sequence 3879, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3879:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-3879

Query Match      60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 17 CCCAGTTGAAGT 6

RESULT 27
US-08-584-040-3880/c
; Sequence 3880, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3880:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-3880

Query Match 60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||
DB 16 CCCAGTTGAAGT 5

RESULT 28

US-09-371-772B-1646/c
; Sequence 1646, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1646

Query Match 60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||
DB 17 CCCAGTTGAAGT 6

RESULT 29

US-09-371-772B-1647/c
; Sequence 1647, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1647

Query Match 60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||
DB 16 CCCAGTTGAAGT 5

RESULT 30

US-09-371-772B-6253/c
; Sequence 6253, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6253
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6253

Query Match 60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||
DB 15 CCCAGTTGAAGT 4

RESULT 31

US-09-371-772B-6254/c
; Sequence 6254, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6254
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6254

Query Match 60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
| | | | | | | | | | | | | | | | |
Db 12 CCCAGTTGAAGT 1

RESULT 32
US-09-685-664B-1646/c
; Sequence 1646, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1646

Query Match 60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
| | | | | | | | | | | | | | | | |
Db 17 CCCAGTTGAAGT 6

RESULT 33
US-09-685-664B-1647/c
; Sequence 1647, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1647

Query Match 60.0%; Score 12; DB 3; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
| | | | | | | | | | | | | | | | |
Db 16 CCCAGTTGAAGT 5

RESULT 34
US-10-138-674B-1646/c
; Sequence 1646, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-1646

Query Match 60.0%; Score 12; DB 5; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
| | | | | | | | | | | | | | | | |
Db 17 CCCAGTTGAAGT 6

RESULT 35
US-10-138-674B-1647/c
; Sequence 1647, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

```
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-1647

Query Match          60.0%; Score 12; DB 5; Length 17;
Score over Length    70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
DB 16 CCCAGTTGAAGT 5

RESULT 36
US-10-138-674B-6253/c
; Sequence 6253, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6253
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-6253

Query Match          60.0%; Score 12; DB 5; Length 17;
Score over Length    70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
DB 15 CCCAGTTGAAGT 4

RESULT 37
US-10-138-674B-6254/c
; Sequence 6254, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6254
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; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-6254

Query Match          60.0%; Score 12; DB 5; Length 17;
Score over Length    70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
DB 12 CCCAGTTGAAGT 1

RESULT 38
US-10-138-674B-8571/c
; Sequence 8571, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-8571

Query Match          60.0%; Score 12; DB 5; Length 17;
Score over Length    70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
DB 14 CCCAGTTGAAGT 3

RESULT 39
US-10-310-914B-1191074/c
; Sequence 1191074, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1191074
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1191074

Query Match          67.0%; Score 13.4; DB 6; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 5.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


Qy 4 CCAGTTGAAGTTGCC 18
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Db 17 CCAGTTGAAGTTCCC 3

RESULT 40

US-08-401-512-16
; Sequence 16, Application US/08401512
; Patent No. 5599673
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Curran, Mark E.
; APPLICANT: Wang, Qing
; TITLE OF INVENTION: Long QT Syndrome Genes
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3917
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,512
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 19780-113879
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-401-512-16

Query Match 42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCCACTTGA 11
|||||
Db 1 CCCCACTGA 10

RESULT 41

US-08-738-381-48/c
; Sequence 48, Application US/08738381
; Patent No. 6083694
; GENERAL INFORMATION:
; APPLICANT: John A. Hardy, Alison M. Goate
; TITLE OF INVENTION: Method for Elucidation and
; TITLE OF INVENTION: Detection of Polymorphisms, Splice Variants and
; TITLE OF INVENTION: Proximal Coding Using Intronic Sequences of the
; TITLE OF INVENTION: Mutations Alzheimer's S182 Gene
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation

; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,381
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,048
; FILING DATE: October 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: P50388
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-08-738-381-48

Query Match 42.0%; Score 8.4; DB 3; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
|||||
Db 10 GTTGATGTTG 1

RESULT 42

US-10-078-958-50/c
; Sequence 50, Application US/10078958
; Patent No. 7064244
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-078-958-50

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10
| | | | | | | |
Db 12 GCCCCAGTAG 3

RESULT 43

US-10-078-958-59/c
; Sequence 59, Application US/10078958
; Patent No. 7064244
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vx REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-078-958-59

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10
| | | | | | | |
Db 12 GCCCCAGTAG 3

Search completed: December 3, 2007, 17:46:21
Job time : 223 secs

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:28:31 ; Search time 6392 Seconds

(without alignments)
74.253 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagtgagtgccgt 20

Scoring table: Oligo_NUC

Gapop 60.0 , Gapext 60.0

Searched: 31364175 seqs, 1186555624 residues

Word size : 1

Total number of hits satisfying chosen parameters: 37000596

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
- 17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*
- 18: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 19: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq:*
- 20: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11C_PUBCOMB.seq:*
- 21: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11D_PUBCOMB.seq:*
- 22: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq:*
- 23: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11F_PUBCOMB.seq:*
- 24: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq:*
- 25: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq:*
- 26: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq:*
- 27: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-908-147-64
2	20	100.0	20	9	US-10-728-509-64
3	18	90.0	20	3	US-09-908-147-65
4	18	90.0	20	9	US-10-728-509-65
5	16	80.0	20	3	US-09-908-147-119
6	16	80.0	20	9	US-10-728-509-119

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTTCGGT 20
DB 1 GCCCCAGTTGAAGTTCGGT 20

ALIGNMENTS

RESULT 1
US-09-908-147-64
; Sequence 64, Application US/09908147
; Publication No. US2003014221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-64

7 15 75.0 18 3 US-09-908-147-5
8 15 75.0 18 9 US-10-728-509-5
9 15 75.0 25 12 US-10-932-182A-95621
10 15 75.0 25 21 US-11-217-529-95621
c 11 14 70.0 19 15 US-10-714-333A-764639
c 12 14 70.0 19 19 US-11-083-784-764639
c 13 14 70.0 19 20 US-11-101-244-764639
c 14 14 70.0 25 9 US-10-719-956-88092
c 15 14 70.0 25 9 US-10-719-956-179809
c 16 14 70.0 25 18 US-11-036-317-560158
c 17 14 70.0 25 20 US-11-121-849-128967
c 18 14 70.0 25 20 US-11-121-849-128967
c 19 14 70.0 25 23 US-11-371-354-19250
c 20 14 70.0 33 24 US-11-406-880B-596981
c 21 14 70.0 37 8 US-10-331-907-146
c 22 13 65.0 19 15 US-10-714-333A-726378
c 23 13 65.0 19 15 US-10-714-333A-726385
c 24 13 65.0 19 15 US-10-714-333A-805351
c 25 13 65.0 19 15 US-10-714-333A-805410
c 26 13 65.0 19 15 US-10-714-333A-1208394
c 27 13 65.0 19 15 US-10-714-333A-1208423
c 28 13 65.0 19 15 US-10-714-333A-1546246
c 29 13 65.0 19 19 US-11-083-784-726378
c 30 13 65.0 19 19 US-11-083-784-726385
c 31 13 65.0 19 19 US-11-083-784-805351
c 32 13 65.0 19 19 US-11-083-784-805410
c 33 13 65.0 19 19 US-11-083-784-1208394
c 34 13 65.0 19 19 US-11-083-784-1208423
c 35 13 65.0 19 19 US-11-083-784-1546246
c 36 13 65.0 19 20 US-11-101-244-726378
c 37 13 65.0 19 20 US-11-101-244-726385
c 38 13 65.0 19 20 US-11-101-244-805351
c 39 13 65.0 19 20 US-11-101-244-805410
c 40 13 65.0 19 20 US-11-101-244-1208394
c 41 13 65.0 19 20 US-11-101-244-1208423
c 42 13 65.0 19 20 US-11-101-244-1546246
c 43 13 65.0 20 3 US-09-908-147-118
c 44 13 65.0 20 8 US-09-908-147-120
c 45 13 65.0 20 8 US-10-932-585-5524

Sequence 5, Appli
Sequence 5, Appli
Sequence 95621, A
Sequence 95621, A
Sequence 764639,
Sequence 764639,
Sequence 88092, A
Sequence 179809,
Sequence 560158,
Sequence 128967,
Sequence 128967,
Sequence 19250, A
Sequence 596981,
Sequence 146, App
Sequence 726378,
Sequence 726385,
Sequence 805351,
Sequence 805410,
Sequence 1208394,
Sequence 1208423,
Sequence 1546246,
Sequence 726378,
Sequence 726385,
Sequence 805351,
Sequence 805410,
Sequence 1208394,
Sequence 1208423,
Sequence 1546246,
Sequence 726378,
Sequence 726385,
Sequence 805351,
Sequence 805410,
Sequence 1208394,
Sequence 1208423,
Sequence 1546246,
Sequence 118, App
Sequence 120, App
Sequence 5524, Ap

RESULT 2

US-10-728-509-64
; Sequence 64, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-64

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTGGCGT 20
|||
Db 1 GCCCCAGTTGAAGTGGCGT 20

RESULT 3

US-09-908-147-65
; Sequence 65, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-65

Query Match 90.0%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTGGCC 18
|||
Db 3 GCCCCAGTTGAAGTGGCC 20

RESULT 4

US-10-728-509-65
; Sequence 65, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17

; NUMBER OF SEQ ID NOS: 168

; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-65

Query Match 90.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTGGCC 18
|||
Db 3 GCCCCAGTTGAAGTGGCC 20

RESULT 5

US-09-908-147-119
; Sequence 119, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-119

Query Match 80.0%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTGGCC 18
|||
Db 1 CCCAGTTGAAGTGGCC 16

RESULT 6

US-10-728-509-119
; Sequence 119, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-119

Query Match 80.0%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCC 18
|||||
Db 1 CCCAGTTGAAGTTGCC 16

RESULT 7

US-09-908-147-5
; Sequence 5, Application US/09908147
; Publication No. US2003014221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-908-147-5

Query Match 75.0%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
|||||
Db 4 GCCCCAGTTGAAGTT 18

RESULT 8

US-10-728-509-5
; Sequence 5, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-728-509-5

Query Match 75.0%; Score 15; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
|||||
Db 4 GCCCCAGTTGAAGTT 18

RESULT 9

US-10-932-182A-95621
; Sequence 95621, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-95621

Query Match 75.0%; Score 15; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGC 17
|||||
Db 10 CCCAGTTGAAGTTGC 24

RESULT 10

US-11-217-529-95621
; Sequence 95621, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-95621

Query Match 75.0%; Score 15; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGC 17
|||||
Db 10 CCCAGTTGAAGTTGC 24

RESULT 11

US-10-714-333A-764639/c
; Sequence 764639, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050

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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-764639

Query Match          70.0%; Score 14; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 12
US-11-083-784-764639/c
; Sequence 764639, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-764639

Query Match          70.0%; Score 14; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 13
US-11-101-244-764639/c
; Sequence 764639, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-764639

Query Match          70.0%; Score 14; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 14
US-10-719-956-88092
; Sequence 88092, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-88092

Query Match          70.0%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
Db 9 CCAGTTGAAGTTGC 22

RESULT 15
US-10-719-956-179809/c
; Sequence 179809, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 179809
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-179809

Query Match          70.0%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 7 GTTGAAGTTGCCGT 20
| | | | | | | | | |
Db 21 GTTGAAGTTGCCGT 8

Search completed: December 3, 2007, 18:15:06
Job time : 6395 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:33:10 ; Search time 754 Seconds
(without alignments)
25.967 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagtgaagttgccgt 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2833015 seqs, 489481754 residues

Word size : 1

Total number of hits satisfying chosen parameters: 4885892

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /EMC Celerra_SIDS2/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC Celerra_SIDS2/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC Celerra_SIDS2/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC Celerra_SIDS2/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC Celerra_SIDS2/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC Celerra_SIDS2/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC Celerra_SIDS2/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC Celerra_SIDS2/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /EMC Celerra_SIDS2/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14	70.0	19	8	US-11-095-383-764639
C 2	14	70.0	25	7	US-11-095-599-593353
C 3	13	65.0	19	8	US-11-095-383-726378
C 4	13	65.0	19	8	US-11-095-383-726385
C 5	13	65.0	19	8	US-11-095-383-805351
C 6	13	65.0	19	8	US-11-095-383-805410
C 7	13	65.0	19	8	US-11-095-383-1208394
C 8	13	65.0	19	8	US-11-095-383-1208423
C 9	13	65.0	19	8	US-11-095-383-1546246
C 10	13	65.0	25	7	US-11-095-599-241845
C 11	13	65.0	25	7	US-11-095-599-268739
C 12	13	65.0	25	7	US-11-095-599-607730
C 13	12	60.0	19	8	US-11-095-383-4103
C 14	12	60.0	19	8	US-11-095-383-726390
C 15	12	60.0	19	8	US-11-095-383-1132462
C 16	12	60.0	19	8	US-11-095-383-1132508
C 17	12	60.0	19	8	US-11-095-383-1208461
C 18	12	60.0	19	8	US-11-095-383-1250562
C 19	12	60.0	25	7	US-11-095-599-68029
C 20	12	60.0	25	7	US-11-095-599-127413
C 21	12	60.0	25	7	US-11-095-599-177427
C 22	12	60.0	25	7	US-11-095-599-288862
C 23	12	60.0	25	7	US-11-095-599-352349
C 24	12	60.0	25	7	US-11-095-599-357863

C 25	12	60.0	25	7	US-11-095-599-487464	Sequence 487464,
C 26	12	60.0	29	7	US-11-095-603-928	Sequence 928, App
C 27	12	60.0	29	7	US-11-095-603-928	Sequence 928, App
C 28	12	60.0	29	7	US-11-095-579-928	Sequence 928, App
C 29	12	60.0	29	7	US-11-095-610-928	Sequence 928, App
C 30	12	60.0	29	7	US-11-095-598-928	Sequence 928, App
C 31	11	55.0	19	6	US-10-553-729-821	Sequence 821, App
C 32	11	55.0	19	6	US-10-553-729-2472	Sequence 2472, App
C 33	11	55.0	19	8	US-11-095-383-4169	Sequence 4169, App
C 34	11	55.0	19	8	US-11-095-383-64620	Sequence 64620, A
C 35	11	55.0	19	8	US-11-095-383-104611	Sequence 104611,
C 36	11	55.0	19	8	US-11-095-383-104627	Sequence 104627,
C 37	11	55.0	19	8	US-11-095-383-189244	Sequence 189244,
C 38	11	55.0	19	8	US-11-095-383-189290	Sequence 189290,
C 39	11	55.0	19	8	US-11-095-383-208863	Sequence 208863,
C 40	11	55.0	19	8	US-11-095-383-236981	Sequence 236981,
C 41	11	55.0	19	8	US-11-095-383-258320	Sequence 258320,
C 42	11	55.0	19	8	US-11-095-383-258408	Sequence 258408,
C 43	11	55.0	19	8	US-11-095-383-265304	Sequence 265304,
C 44	11	55.0	19	8	US-11-095-383-265334	Sequence 265334,
C 45	11	55.0	19	8	US-11-095-383-265443	Sequence 265443,

ALIGNMENTS

RESULT 1
US-11-095-383-764639/c
; Sequence 764639, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarsdale, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134999US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-764639

Query Match 70.0%; Score 14; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 2
US-11-095-599-593353/c
; Sequence 593353, Application US/11695599
; Publication No. US20070243546A1
; GENERAL INFORMATION:
; APPLICANT: Yan Cao
; APPLICANT: Shivani Nautiyal
; APPLICANT: Garry Miyada
; APPLICANT: Chris Davies


```
; APPLICANT: Gangwu Mei
; APPLICANT: Alan Williams
; APPLICANT: Eric Schell
; APPLICANT: John E. Blume
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays
; FILE REFERENCE: 3791.1
; CURRENT APPLICATION NUMBER: US/11/695,599
; CURRENT FILING DATE: 2007-04-02
; PRIOR APPLICATION NUMBER: 60/788,520
; PRIOR FILING DATE: 2006-03-31
; NUMBER OF SEQ ID NOS: 743256
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 593353
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-695-599-593353

Query Match      70.0%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CCAGTTGAAGTTGCC 17
DB      15 CCAGTTGAAGTTGCC 2

RESULT 3
US-11-095-383-726378/c
; Sequence 726378, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726378
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-726378

Query Match      65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
DB      17 AGTTGAAGTTGCC 5

RESULT 4
US-11-095-383-726385/c
; Sequence 726385, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726378
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-726385

Query Match      65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
DB      17 AGTTGAAGTTGCC 5
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726385
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-726385

Query Match      65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
DB      18 AGTTGAAGTTGCC 6

RESULT 5
US-11-095-383-805351/c
; Sequence 805351, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 805351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-805351

Query Match      65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTGCCGT 20
DB      15 TTGAAGTTGCCGT 3

RESULT 6
US-11-095-383-805410/c
; Sequence 805410, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 805410
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-805410
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Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 8 TTGAAGTTGCCGT 20
Db 14 TTGAAGTTGCCGT 2
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RESULT 7

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US-11-095-383-1208394/c
; Sequence 1208394, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1208394
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-1208394
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Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 CCAGTTGAAGTTG 16
Db 16 CCAGTTGAAGTTG 4
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RESULT 8

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US-11-095-383-1208423/c
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; Sequence 1208423, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1208423
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-1208423
```

```
Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 CCAGTTGAAGTTG 16
Db 17 CCAGTTGAAGTTG 5
```

RESULT 9

```
US-11-095-383-1546246/c
; Sequence 1546246, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1546246
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-1546246
```

```
Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 7 GTTGAAGTTGCCG 19
Db 19 GTTGAAGTTGCCG 7
```

RESULT 10

US-11-695-599-241845/c
; Sequence 241845, Application US/11695599
; Publication No. US20070243546A1
; GENERAL INFORMATION:
; APPLICANT: Yan Cao
; APPLICANT: Shivani Nautiyal
; APPLICANT: Garry Miyada
; APPLICANT: Chris Davies
; APPLICANT: Gangwu Mei
; APPLICANT: Alan Williams
; APPLICANT: Eric Schell
; APPLICANT: John E. Blume
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays
; FILE REFERENCE: 3791.1
; CURRENT APPLICATION NUMBER: US/11/695,599
; CURRENT FILING DATE: 2007-04-02
; PRIOR APPLICATION NUMBER: 60/788,520
; PRIOR FILING DATE: 2006-03-31
; NUMBER OF SEQ ID NOS: 743256
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 241845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-695-599-241845

Query Match 65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTCGCGT 20
| | | | | | | | | |
DB 16 TTGAAGTTCGCGT 4

RESULT 11

US-11-695-599-268739/c
; Sequence 268739, Application US/11695599
; Publication No. US20070243546A1
; GENERAL INFORMATION:
; APPLICANT: Yan Cao
; APPLICANT: Shivani Nautiyal
; APPLICANT: Garry Miyada
; APPLICANT: Chris Davies
; APPLICANT: Gangwu Mei
; APPLICANT: Alan Williams
; APPLICANT: Eric Schell
; APPLICANT: John E. Blume
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays
; FILE REFERENCE: 3791.1
; CURRENT APPLICATION NUMBER: US/11/695,599
; CURRENT FILING DATE: 2007-04-02
; PRIOR APPLICATION NUMBER: 60/788,520
; PRIOR FILING DATE: 2006-03-31
; NUMBER OF SEQ ID NOS: 743256
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 268739
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-695-599-268739

Query Match 65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
| | | | | | | | | |
DB 19 GCCCCAGTTGAAG 7

RESULT 12

US-11-695-599-607730/c
; Sequence 607730, Application US/11695599
; Publication No. US20070243546A1
; GENERAL INFORMATION:
; APPLICANT: Yan Cao
; APPLICANT: Shivani Nautiyal
; APPLICANT: Garry Miyada
; APPLICANT: Chris Davies
; APPLICANT: Gangwu Mei
; APPLICANT: Alan Williams
; APPLICANT: Eric Schell
; APPLICANT: John E. Blume
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays
; FILE REFERENCE: 3791.1
; CURRENT APPLICATION NUMBER: US/11/695,599
; CURRENT FILING DATE: 2007-04-02
; PRIOR APPLICATION NUMBER: 60/788,520
; PRIOR FILING DATE: 2006-03-31
; NUMBER OF SEQ ID NOS: 743256
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 607730
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-695-599-607730

Query Match 65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTT 15
| | | | | | | | | |
DB 25 CCCAGTTGAAGTT 13

RESULT 13

US-11-095-383-4103/c
; Sequence 4103, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarsinge, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 4103
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-4103

Query Match 60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
| | | | | | | | | |
DB 12 CAGTTGAAGTTG 1

RESULT 14

US-11-095-383-726390/c
; Sequence 726390, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726390
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-726390

Query Match 60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred.No. 6.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18

Db 19 GTTGAAGTTGCC 8

RESULT 15

US-11-095-383-1132462/c
; Sequence 1132462, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1132462
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-1132462

Query Match 60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred.No. 6.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCC 19

Db 18 TTGAAGTTGCC 7
Search completed: December 3, 2007, 16:58:28
Job time : 755 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:22:33 ; Search time 206 Seconds
(without alignments)
72.858 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagttgaagttgccgt 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 614577 seqs, 375217992 residues

Word size: 1

Total number of hits satisfying chosen parameters: 433342

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database: Pending Patents NA New:*

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- 2: /EMC_Celerra_SIDS2/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /EMC_Celerra_SIDS2/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /EMC_Celerra_SIDS2/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /EMC_Celerra_SIDS2/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /EMC_Celerra_SIDS2/ptodata/2/pna/US10_NEW_COMB.seq:*
- 7: /EMC_Celerra_SIDS2/ptodata/2/pna/US11_NEW_COMB.seq:*
- 8: /EMC_Celerra_SIDS2/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16	80.0	22	1	PCT-US07-11121-41
c 2	12	60.0	32	7	US-11-884-818-26
c 3	12	60.0	32	7	US-11-884-818-29
c 4	12	60.0	35	7	US-11-909-031-55
c 5	11	55.0	19	7	US-11-977-128-13195
c 6	11	55.0	19	7	US-11-977-128-21540
c 7	11	55.0	20	8	US-60-986-286-208
c 8	11	55.0	21	6	US-10-923-3798B-1922
c 9	11	55.0	21	6	US-10-923-3798B-1923
c 10	11	55.0	21	6	US-10-923-3798B-1950
c 11	11	55.0	21	6	US-10-923-3798B-1951
c 12	11	55.0	21	6	US-10-923-3798B-1978
c 13	11	55.0	21	6	US-10-923-3798B-1979
c 14	11	55.0	21	6	US-10-923-3798B-2006
c 15	11	55.0	21	6	US-10-923-3798B-2007
c 16	11	55.0	21	6	US-10-923-3798B-2034
c 17	11	55.0	21	6	US-10-923-3798B-2035
c 18	11	55.0	21	6	US-10-923-3798B-2062
c 19	11	55.0	21	6	US-10-923-3798B-2063
c 20	11	55.0	21	6	US-10-923-3798B-2090
c 21	11	55.0	21	6	US-10-923-3798B-2091
c 22	11	55.0	21	6	US-10-923-3798B-2118
c 23	11	55.0	21	6	US-10-923-3798B-2119
c 24	11	55.0	21	6	US-10-923-3798B-2146
c 25	11	55.0	21	6	US-10-923-3798B-2147

26	11	55.0	21	6	US-10-923-3798B-2174	Sequence 2174, Ap
27	11	55.0	21	6	US-10-923-3798B-2175	Sequence 2175, Ap
28	11	55.0	21	6	US-10-923-3798B-2202	Sequence 2202, Ap
29	11	55.0	21	6	US-10-923-3798B-2203	Sequence 2203, Ap
30	11	55.0	21	6	US-10-923-3798B-2230	Sequence 2230, Ap
31	11	55.0	21	6	US-10-923-3798B-2231	Sequence 2231, Ap
32	11	55.0	21	7	US-11-746-864-532	Sequence 532, App
33	11	55.0	21	7	US-11-746-864-534	Sequence 534, App
c 34	11	55.0	23	6	US-10-923-3798B-1508	Sequence 1508, Ap
c 35	11	55.0	23	6	US-10-923-3798B-1509	Sequence 1509, Ap
c 36	11	55.0	29	7	US-11-737-025-34	Sequence 34, Appl
c 37	11	55.0	33	7	US-11-836-770-11	Sequence 11, Appl
c 38	11	55.0	40	6	US-10-548-533-5	Sequence 5, Appli
c 39	10	50.0	19	7	US-11-001-347B-592	Sequence 592, App
c 40	10	50.0	19	7	US-11-001-347B-763	Sequence 763, App
c 41	10	50.0	19	7	US-11-977-128-660	Sequence 660, App
c 42	10	50.0	19	7	US-11-977-128-16883	Sequence 16883, A
c 43	10	50.0	19	8	US-60-956-679-75	Sequence 75, Appl
c 44	10	50.0	19	8	US-60-934-954-153	Sequence 153, App
c 45	10	50.0	20	6	US-10-576-900-175	Sequence 175, App

ALIGNMENTS

RESULT 1

PCT-US07-11121-41/c
; Sequence 41, Application PC/TUS0711121
; GENERAL INFORMATION:
; APPLICANT: Hitachi Chemical Co., Ltd.
; APPLICANT: Hitachi Chemical Research Center, Inc.
; APPLICANT: Mitsuhashi, Masato
; APPLICANT: Ibara, Kazuhiko
; TITLE OF INVENTION: Method for Testing Drug Sensitivity in
; TITLE OF INVENTION: Solid Tumors by Quantifying mRNA Expression in Thinly-Sliced
; TITLE OF INVENTION: Tumor Tissue
; FILE REFERENCE: HITACHI.081VPC
; CURRENT APPLICATION NUMBER: PCT/US07/11121
; CURRENT FILING DATE: 2007-09-19
; PRIOR APPLICATION NUMBER: PCT/US2007/011121
; PRIOR FILING DATE: 2007-05-08
; PRIOR APPLICATION NUMBER: US 60/798,674
; PRIOR FILING DATE: 2006-05-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BAX forward primer sequence
PCT-US07-11121-41

Query Match 80.0%; Score 16; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTCGGT 20

DB 22 CAGTTGAAGTTCGGT 7

RESULT 2

US-11-884-818-26
; Sequence 26, Application US/11884818
; GENERAL INFORMATION:
; APPLICANT: Duwenig, Elke
; APPLICANT: Loyall, Linda P
; TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS
; FILE REFERENCE: 13987-00085-US
; CURRENT APPLICATION NUMBER: US/11/884,818
; CURRENT FILING DATE: 2007-09-06
; PRIOR APPLICATION NUMBER: PCT/EP2006/060266

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; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 05004248.0
; PRIOR FILING DATE: 2005-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.4
; SEQ ID NO 26
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-11-884-818-26

Query Match          60.0%; Score 12; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 16 AGTTGAAGTTGC 27

RESULT 3
US-11-884-818-29
; Sequence 29, Application US/11884818
; GENERAL INFORMATION:
; APPLICANT: Duwengig, Elke
; APPLICANT: Loyall, Linda P
; TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS
; FILE REFERENCE: 13987-00065-US
; CURRENT APPLICATION NUMBER: US/11/884,818
; CURRENT FILING DATE: 2007-09-06
; PRIOR APPLICATION NUMBER: PCT/EP2006/060266
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 05004248.0
; PRIOR FILING DATE: 2005-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.4
; SEQ ID NO 29
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-11-884-818-29

Query Match          60.0%; Score 12; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 16 AGTTGAAGTTGC 27

RESULT 4
US-11-909-031-55
; Sequence 55, Application US/11909031
; GENERAL INFORMATION:
; APPLICANT: Astellas Pharma Inc.
; APPLICANT: ENDOH, Hideki
; APPLICANT: YOKOTA, Hiroyuki
; APPLICANT: HAYAKAWA, Masahiko
; APPLICANT: SOGA, Shinji
; TITLE OF INVENTION: A method for identification of drug targets and a method of
; screening antidiabetic drug using the identified target
; FILE REFERENCE: Q10930
; CURRENT APPLICATION NUMBER: US/11/909,031
; CURRENT FILING DATE: 2007-09-18
; PRIOR APPLICATION NUMBER: JP2005-234673
; PRIOR FILING DATE: 2005-08-12
; PRIOR APPLICATION NUMBER: JP2005-279582
; PRIOR FILING DATE: 2005-09-27
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; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer sequence
US-11-909-031-55

Query Match          60.0%; Score 12; DB 7; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
Db 10 CAGTTGAAGTTG 21

RESULT 5
US-11-977-128-13195
; Sequence 13195, Application US/11977128
; GENERAL INFORMATION:
; APPLICANT: KHVOROVA, Anastasia
; APPLICANT: REYNOLDS, Angela
; APPLICANT: LEAKE, Devin
; APPLICANT: MARSHALL, William
; APPLICANT: READ, Steven
; APPLICANT: SCARINGE, Stephen
; TITLE OF INVENTION: siRNA Targeting Kinases
; FILE REFERENCE: DHARMA 2100-US74
; CURRENT APPLICATION NUMBER: US/11/977,128
; CURRENT FILING DATE: 2007-10-31
; PRIOR APPLICATION NUMBER: 10/940,892
; PRIOR FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: PCT/US04/14885
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,136
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 22603
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-977-128-13195

Query Match          55.0%; Score 11; DB 7; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.3e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 7 AGUUGAAGUUG 17

RESULT 6
US-11-977-128-21540
; Sequence 21540, Application US/11977128
; GENERAL INFORMATION:
; APPLICANT: KHVOROVA, Anastasia
; APPLICANT: REYNOLDS, Angela
; APPLICANT: LEAKE, Devin
; APPLICANT: MARSHALL, William
; APPLICANT: READ, Steven
; APPLICANT: SCARINGE, Stephen
; TITLE OF INVENTION: siRNA Targeting Kinases
```

; FILE REFERENCE: DHARMA 2100-US74
; CURRENT APPLICATION NUMBER: US/11/977,128
; CURRENT FILING DATE: 2007-10-31
; PRIOR APPLICATION NUMBER: 10/940,892
; PRIOR FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: PCT/US04/14885
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,136
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 22603
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21540
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-11-977-128-21540

Query Match 55.0%; Score 11; DB 7; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.3e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
||:||||:
Db 2 AGUUGAAGUG 12

RESULT 7
US-60-986-286-208/c
; Sequence 208, Application US/60986286
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Kristina Lemonidis Tarbet
; APPLICANT: Sanjay Bhanot
; APPLICANT: Diane Tribble
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: METHODS FOR TREATING
; TITLE OF INVENTION: HYPERCHOLESTEROLEMIA
; FILE REFERENCE: BIOL0090US.L3
; CURRENT APPLICATION NUMBER: US/60/986,286
; CURRENT FILING DATE: 2007-11-07
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-60-986-286-208

Query Match 55.0%; Score 11; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCC 18
|||||
Db 11 TTGAAGTTGCC 1

RESULT 8
US-10-923-379B-1922/c
; Sequence 1922, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haeberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1922
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
; OTHER INFORMATION: sequence
; US-10-923-379B-1922

Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGC 17
|||||
Db 18 GTTGAAGTTGC 8

RESULT 9
US-10-923-379B-1923/c
; Sequence 1923, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haeberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1923
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
; OTHER INFORMATION: sequence
; US-10-923-379B-1923

Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGC 17
|||||
Db 17 GTTGAAGTTGC 7

RESULT 10
US-10-923-379B-1950
; Sequence 1950. Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1950
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
; OTHER INFORMATION: sequence
US-10-923-379B-1950

Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 63.6%; Pred. No. 1.3e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGC 17
|:|||||:
Db 2 GUUGAAGUUGC 12

RESULT 11
US-10-923-379B-1951
; Sequence 1951. Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1951
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
; OTHER INFORMATION: sequence
US-10-923-379B-1951

Query Match 55.0%; Score 11; DB 6; Length 21;

Best Local Similarity 63.6%; Pred. No. 1.3e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGC 17
|:|||||:
Db 3 GUUGAAGUUGC 13

RESULT 12
US-10-923-379B-1978/c
; Sequence 1978. Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1978
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(6)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety
US-10-923-379B-1978

Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGC 17
|:|||||:
Db 18 GTTGAAGTTGC 8

RESULT 13


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US-10-923-379B-1979/c
; Sequence 1979, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1979
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
US-10-923-379B-1979
;
; Query Match 55.0%; Score 11; DB 6; Length 21;
; Best Local Similarity 100.0%; Pred. No. 1.3e+03;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 7 GTTGAAGTTGC 17
DB 17 GTTGAAGTTGC 7
;
RESULT 14
US-10-923-379B-2006
; Sequence 2006, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2007
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (3)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: internucleotide phosphorothioate linkage
; OTHER INFORMATION: sequence
US-10-923-379B-2006
;
; Query Match 55.0%; Score 11; DB 6; Length 21;
; Best Local Similarity 63.6%; Pred. No. 1.3e+03;
; Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
;
QY 7 GTTGAAGTTGC 17
DB 2 GUUGAAGUUGC 12
;
RESULT 15
US-10-923-379B-2007
; Sequence 2007, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2007
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2006
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (3)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: internucleotide phosphorothioate linkage
; OTHER INFORMATION: sequence
US-10-923-379B-2006
;
; Query Match 55.0%; Score 11; DB 6; Length 21;
; Best Local Similarity 63.6%; Pred. No. 1.3e+03;
; Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
;
QY 7 GTTGAAGTTGC 17
DB 2 GUUGAAGUUGC 12
;
RESULT 15
US-10-923-379B-2007
; Sequence 2007, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2007
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: internucleotide phosphorothioate linkage
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
; OTHER INFORMATION: sequence
US-10-923-379B-2007
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Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 63.6%; Pred. NO. 1.3e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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QY 7 GTTGAAGTTGC 17
Db 3 GUUGAAGUUGC 13
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Search completed: December 3, 2007, 16:25:59
Job time : 206 secs
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GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:39:38 ; Search time 457 Seconds

(without alignments)

472.446 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagtgaagtgcgt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 284

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum Score over Length 70%

Listing first 1000 summaries

Database : N Geneseq 200711.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000.*

4: Geneseqn2001a.*

5: Geneseqn2001b.*

6: Geneseqn2002a.*

7: Geneseqn2002b.*

8: Geneseqn2003a.*

9: Geneseqn2003b.*

10: Geneseqn2003c.*

11: Geneseqn2003d.*

12: Geneseqn2004a.*

13: Geneseqn2004b.*

14: Geneseqn2004c.*

15: Geneseqn2004d.*

16: Geneseqn2005a.*

17: Geneseqn2005b.*

18: Geneseqn2005c.*

19: Geneseqn2006a.*

20: Geneseqn2006b.*

21: Geneseqn2006c.*

22: Geneseqn2007.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	over Length	Query Match	Length	ID	Description
1	20	100.0	100.0	20	8	ADA20891 Hu
2	18	90.0	90.0	20	8	ADA20892 Hu
3	15	83.3	75.0	18	8	ADA20832 Hu
C 4	10	83.3	50.0	12	5	ABH71796 Ol
C 5	10	83.3	50.0	12	5	ABH74771 Ol
6	10	83.3	50.0	12	5	ABH53278 Ol
C 7	10	83.3	50.0	12	5	ABH41500 Ol
8	10	83.3	50.0	12	5	ABH10235 Ol
C 9	10	83.3	50.0	12	5	ABH15838 Ol
10	16.4	82.0	82.0	20	8	ADA20946 Mo
11	11.4	81.4	57.0	14	2	AAQ83299 c-
12	16	80.0	80.0	20	8	ABX13068 Hu

13	16	80.0	80.0	20	17	ABD12216	Ba
14	16	80.0	80.0	20	19	AEJ97326	RT
15	16	80.0	80.0	20	19	AEK58344	In
C 16	12	80.0	60.0	15	2	AAX75721	Hu
17	10.4	80.0	52.0	13	5	ABF87034	Ol
C 18	10.4	80.0	52.0	13	5	ABF87035	Ol
C 19	9.4	78.3	47.0	12	5	ABF37784	Ol
C 20	9.4	78.3	47.0	12	5	ABF45117	Ol
C 21	9.4	78.3	47.0	12	5	ABH82576	Ol
22	9.4	78.3	47.0	12	5	ABH29461	Ol
23	9.4	78.3	47.0	12	5	ABH05273	Ol
24	9.4	78.3	47.0	12	5	ABH161450	Ol
25	9.4	78.3	47.0	12	5	ABH00657	Ol
C 26	9.4	78.3	47.0	12	5	ABH81979	Ol
C 27	9.4	78.3	47.0	12	5	ABH39385	Ol
C 28	9.4	78.3	47.0	12	5	ABH80268	Ol
29	9.4	78.3	47.0	12	5	ABH14375	Ol
C 30	9.4	78.3	47.0	12	5	ABH75142	Ol
31	9.4	78.3	47.0	12	22	AEH30648	E
32	9.4	78.3	47.0	12	22	AEH30671	E
C 33	17	77.3	85.0	22	7	ABV73748	Hu
C 34	10	76.9	50.0	13	2	AAZ21922	Fr
C 35	10	76.9	50.0	13	5	ABF31261	Ol
C 36	10	76.9	50.0	13	5	ABF71654	Ol
C 37	10	76.9	50.0	13	5	ABF50115	Ol
C 38	10	76.9	50.0	13	5	ABF07779	Ol
C 39	10	76.9	50.0	13	5	ABC65593	Ol
40	10	76.9	50.0	13	5	ABF07778	Ol
C 41	10	76.9	50.0	13	5	ABC28727	Ol
C 42	10	76.9	50.0	13	5	ABF71655	Ol
43	10	76.9	50.0	13	5	ABC28726	Ol
44	10	76.9	50.0	13	5	ABC65592	Ol
C 45	10	76.9	50.0	13	5	ABF53415	Ol
46	10	76.9	50.0	13	5	ABF53414	Ol
47	10	76.9	50.0	13	5	ABF31260	Ol
48	10	76.9	50.0	13	5	ABF50114	Ol
49	10	76.9	50.0	13	16	AEQ4526	Hu
50	10	76.9	50.0	13	19	AEH12245	Hu
51	10	76.9	50.0	13	22	AGI70514	Hu
C 52	9	75.0	45.0	12	5	ABH38653	Ol
C 53	9	75.0	45.0	12	5	ABH43950	Ol
54	9	75.0	45.0	12	5	ABH33999	Ol
55	9	75.0	45.0	12	5	ABH69281	Ol
56	9	75.0	45.0	12	5	ABH42808	Ol
57	9	75.0	45.0	12	5	ABH72541	Ol
58	9	75.0	45.0	12	5	ABH88159	Ol
59	9	75.0	45.0	12	5	ABH98609	Ol
60	9	75.0	45.0	12	5	ABH37700	Ol
61	9	75.0	45.0	12	5	ABH79970	Ol
62	9	75.0	45.0	12	5	ABH98752	Ol
63	9	75.0	45.0	12	5	ABH10039	Ol
C 64	9	75.0	45.0	12	5	ABH19673	Ol
C 65	9	75.0	45.0	12	5	ABH81377	Ol
C 66	9	75.0	45.0	12	5	ABH65921	Ol
C 67	9	75.0	45.0	12	5	ABH32591	Ol
C 68	9	75.0	45.0	12	5	ABH84637	Ol
C 69	9	75.0	45.0	12	5	ABH45848	Ol
C 70	9	75.0	45.0	12	5	ABH08021	Ol
71	9	75.0	45.0	12	5	ABH58136	Ol
72	9	75.0	45.0	12	5	ABH99938	Ol
C 73	9	75.0	45.0	12	5	ABH103368	Ol
C 74	9	75.0	45.0	12	5	ABH38557	Ol
C 75	9	75.0	45.0	12	5	ABH60242	Ol
C 76	9	75.0	45.0	12	5	ABH05053	Ol
C 77	9	75.0	45.0	12	5	ABH69662	Ol
78	9	75.0	45.0	12	6	ABK72546	Hu
C 79	10.4	74.3	52.0	14	2	AAX34784	Ne
80	9.6	73.8	48.0	13	5	ABH61646	Ol
C 81	9.6	73.8	48.0	13	5	ABH61647	Ol
C 82	11	73.3	55.0	15	2	AAX75746	Hu
C 83	11	73.3	55.0	15	3	AAX64449	Su
C 84	11	73.3	55.0	15	6	ABH76210	He
C 85	11	73.3	55.0	15	6	ABX01502	He

c 86	11	73.3	55.0	15	8	ABQ77353	Abq77353 Re	c 159	8.4	70.0	42.0	12	2	AAT93676	Aat93676 Ex
c 87	8.8	73.3	44.0	12	2	AAQ88636	AAQ88636 Hu	c 160	8.4	70.0	42.0	12	2	AAV42278	Aav42278 Cl
c 88	8.8	73.3	44.0	12	2	AAQ88635	AAQ88635 Hu	c 161	8.4	70.0	42.0	12	2	AAV42254	Aav42254 Cl
c 89	8.8	73.3	44.0	12	2	AAZ30061	AAZ30061 Sp	c 162	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 90	8.8	73.3	44.0	12	4	AAZ31364	AAZ31364 In	c 163	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 91	8.8	73.3	44.0	12	4	AAZ31364	AAZ31364 In	c 164	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 92	8.8	73.3	44.0	12	4	AAZ302762	AAZ302762 Hu	c 165	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 93	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 166	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 94	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 167	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 95	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 168	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 96	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 169	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 97	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 170	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 98	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 171	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 99	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 172	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 100	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 173	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 101	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 174	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 102	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 175	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 103	8.8	73.3	44.0	12	5	ABH93674	ABH93674 Ol	c 176	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 104	8.8	73.3	44.0	12	8	AAZ52648	AAZ52648 Hu	c 177	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 105	8.8	73.3	44.0	12	17	AE62435	AE62435 Hu	c 178	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 106	8.8	73.3	44.0	12	17	AE62417	AE62417 Hu	c 179	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 107	8.8	73.3	44.0	12	17	AE62419	AE62419 Hu	c 180	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 108	8.8	73.3	44.0	12	19	AELO3638	AELO3638 Hu	c 181	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 109	8.8	73.3	44.0	12	19	AELO3639	AELO3639 Hu	c 182	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 110	8.8	73.3	44.0	12	22	AELO3631	AELO3631 E.	c 183	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 111	8.8	73.3	44.0	12	22	AGD66526	AGD66526 Hu	c 184	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 112	12.4	72.9	62.0	17	3	AAFO5403	AAFO5403 Ha	c 185	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 113	12.4	72.9	62.0	17	3	AAFO5403	AAFO5403 Ha	c 186	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 114	16	72.7	80.0	22	19	AEH24548	AEH24548 BA	c 187	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 115	16	72.7	80.0	22	19	AEH24560	AEH24560 BA	c 188	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 116	16	72.7	80.0	22	19	AEJ10474	AEJ10474 An	c 189	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 117	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 190	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 118	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 191	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 119	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 192	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 120	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 193	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 121	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 194	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 122	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 195	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 123	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 196	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 124	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 197	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 125	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 198	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 126	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 199	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 127	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 200	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 128	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 201	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 129	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 202	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 130	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 203	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 131	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 204	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 132	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 205	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 133	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 206	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 134	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 207	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 135	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 208	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 136	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 209	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 137	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 210	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 138	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 211	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 139	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 212	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 140	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 213	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 141	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 214	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 142	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 215	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 143	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 216	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 144	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 217	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 145	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 218	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 146	9.4	72.3	47.0	13	5	ABH93674	ABH93674 Ol	c 219	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 147	9.4	72.3	47.0	13	13	ADR35833	ADR35833 Hu	c 220	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 148	9.4	72.3	47.0	13	13	ADR35834	ADR35834 Hu	c 221	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 149	9.4	72.3	47.0	13	13	ADR35835	ADR35835 Hu	c 222	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 150	9.4	72.3	47.0	13	13	ADR35832	ADR35832 Hu	c 223	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 151	12.2	71.8	61.0	17	13	ADQ80013	ADQ80013 A.	c 224	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 152	10	71.4	50.0	14	2	AAQ83300	AAQ83300 C-	c 225	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 153	17	70.8	85.0	24	19	AEJ10477	AEJ10477 Ta	c 226	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 154	17	70.8	85.0	24	19	AEJ10484	AEJ10484 Ta	c 227	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 155	10.6	70.7	53.0	15	6	ABG64186	ABG64186 Ta	c 228	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 156	12	70.6	60.0	17	2	AAAX71130	AAAX71130 Hu	c 229	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 157	12	70.6	60.0	17	2	AAAX71129	AAAX71129 Hu	c 230	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol
c 158	12	70.6	60.0	17	8	ABE61076	ABE61076 Hu	c 231	8.4	70.0	42.0	12	5	ABH93674	Abh93674 Ol

232	8.4	70.0	42.0	12	5	ABI00465	Abi00465 Ol
233	8.4	70.0	42.0	12	5	ABH9246 Ol	Abh9246 Ol
C 234	8.4	70.0	42.0	12	5	ABH88414 Ol	Abh88414 Ol
C 235	8.4	70.0	42.0	12	5	ABI66132 Ol	Abi66132 Ol
C 236	8.4	70.0	42.0	12	5	ABI67005 Ol	Abi67005 Ol
237	8.4	70.0	42.0	12	5	ABI67274 Ol	Abi67274 Ol
C 238	8.4	70.0	42.0	12	5	ABI52749 Ol	Abi52749 Ol
C 239	8.4	70.0	42.0	12	5	ABI16623 Ol	Abi16623 Ol
240	8.4	70.0	42.0	12	5	ABI44330 Ol	Abi44330 Ol
241	8.4	70.0	42.0	12	5	ABI61490 Ol	Abi61490 Ol
242	8.4	70.0	42.0	12	5	ABI74887 Ol	Abi74887 Ol
243	8.4	70.0	42.0	12	5	ABI10236 Ol	Abi10236 Ol
C 244	8.4	70.0	42.0	12	5	ABI31459 Ol	Abi31459 Ol
C 245	8.4	70.0	42.0	12	5	ABI32242 Ol	Abi32242 Ol
C 246	8.4	70.0	42.0	12	5	ABI69897 Ol	Abi69897 Ol
C 247	8.4	70.0	42.0	12	5	ABH92665 Ol	Abh92665 Ol
C 248	8.4	70.0	42.0	12	5	ABI29165 Ol	Abi29165 Ol
C 249	8.4	70.0	42.0	12	5	ABI22105 Ol	Abi22105 Ol
250	8.4	70.0	42.0	12	5	ABH97330 Ol	Abh97330 Ol
C 251	8.4	70.0	42.0	12	5	ABI02630 Ol	Abi02630 Ol
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C 253	8.4	70.0	42.0	12	5	ABI38801 Ol	Abi38801 Ol
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C 258	8.4	70.0	42.0	12	5	ABI47133 Ol	Abi47133 Ol
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C 260	8.4	70.0	42.0	12	5	ABI42212 Ol	Abi42212 Ol
C 261	8.4	70.0	42.0	12	5	ABI61765 Ol	Abi61765 Ol
C 262	8.4	70.0	42.0	12	5	ABI67350 Ol	Abi67350 Ol
263	8.4	70.0	42.0	12	5	ABI80116 Ol	Abi80116 Ol
C 264	8.4	70.0	42.0	12	5	ABH69990 Ol	Abh69990 Ol
265	8.4	70.0	42.0	12	5	ABH95291 Ol	Abh95291 Ol
266	8.4	70.0	42.0	12	5	ABH98049 Ol	Abh98049 Ol
C 267	8.4	70.0	42.0	12	5	ABI33882 Ol	Abi33882 Ol
C 268	8.4	70.0	42.0	12	5	ABI41817 Ol	Abi41817 Ol
C 269	8.4	70.0	42.0	12	5	ABI48505 Ol	Abi48505 Ol
C 270	8.4	70.0	42.0	12	5	ABI76925 Ol	Abi76925 Ol
271	8.4	70.0	42.0	12	5	ABI72013 Ol	Abi72013 Ol
C 272	8.4	70.0	42.0	12	5	ABI58229 Ol	Abi58229 Ol
C 273	8.4	70.0	42.0	12	5	ABI52907 Ol	Abi52907 Ol
C 274	8.4	70.0	42.0	12	5	ABI64624 Ol	Abi64624 Ol
C 275	8.4	70.0	42.0	12	5	ABI62006 Ol	Abi62006 Ol
C 276	8.4	70.0	42.0	12	5	ABI17895 Ol	Abi17895 Ol
C 277	8.4	70.0	42.0	12	5	ABH94593 Ol	Abh94593 Ol
C 278	8.4	70.0	42.0	12	5	ABH96494 Ol	Abh96494 Ol
279	8.4	70.0	42.0	12	5	ABI39317 Ol	Abi39317 Ol
C 280	8.4	70.0	42.0	12	5	ABI52789 Ol	Abi52789 Ol
C 281	8.4	70.0	42.0	12	5	ABI47624 Ol	Abi47624 Ol
C 282	8.4	70.0	42.0	12	5	ABI77409 Ol	Abi77409 Ol
C 283	8.4	70.0	42.0	12	8	ADD69888 Le	Add69888 Le
C 284	8.4	70.0	42.0	12	22	AER38463 Li	Aer38463 Li

ALIGNMENTS

RESULT 1
ADA20891
ID ADA20891 standard; DNA; 20 BP.
XX
AC ADA20891;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:64.
XX
KW BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; ophthalmological; antidiabetic; virocidic;
KW antisense therapy; BAX antagonist; BAX inhibitor;
KW familial amyotrophic lateral sclerosis; Alzheimer's disease;
KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;

Query Match 100.0%; Score 20; DB 8; Length 20;
Score over Length 100.0%;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW diabetes-associated ocular disorder; scrapie infection;
KW aberrant apoptosis; human; phosphorothioate; ss.
XX Synthetic.
OS Homo sapiens.
XX
Key Location/Qualifiers
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/tag= b
/mod_base= OTHER
/notes= "phosphorothioate linkages, and all cytidine
residues are 5-methylcytidines"
modified_base 1..5
/tag= a
/mod_base= OTHER
/notes= "2'-O-methoxyethyls"
modified_base 16..20
/tag= c
/mod_base= OTHER
/notes= "2'-O-methoxyethyls"
WO2003008543-A2.
30-JAN-2003.
13-JUL-2002; 2002WO-US022417.
17-JUL-2001; 2001US-00908147.
(ISIS-) ISIS PHARM INC.
Zhang H, Watt AT;
WPI; 2003-239321/23.
New antisense compounds, useful for modulating the expression of BCL2-
associated X (BAX) protein or for treating a disease or condition
associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
or Alzheimer's disease.
Claim 3; Page 86; 139pp; English.
The present invention describes a compound (I) 8-50 nucleobases in length
targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
protein, where the compound specifically hybridizes with the nucleic acid
molecule encoding BAX protein and inhibits the expression of BAX protein.
The compound specifically hybridizes with at least 8-nucleobase portion
of an active site on a nucleic acid molecule encoding BAX protein. Also
described: (1) a composition comprising (I) and a pharmaceutical carrier
or diluent; (2) inhibiting the expression of BAX protein in cells or
tissues comprising contacting the cells or tissues with (I); and (3)
treating an animal having a disease or condition associated with BAX
protein comprising administering to the animal (I) so that expression of
BAX protein is inhibited. (I) has neurotropic, neuroprotective
antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
virocidic activities, and can be used in antisense therapy, and as a BAX
antagonist. The antisense compounds (I) are useful for modulating the
expression of BAX protein, and for treating a disease or condition
associated with BAX protein, e.g. familial amyotrophic lateral
sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
cartilage-hair hyperplasia, diabetes-associated ocular disorders or
scrapie infection, or a condition that arises from aberrant apoptosis.
The compounds are useful as research reagents and in diagnostics. The
present sequence represents a human BAX chimeric phosphorothioate
oligonucleotide, which is used in an example from the present invention.

Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

QY 1 GCCCCAGTTGAAGTTGCCCT 20
 Db 1 GCCCCAGTTGAAGTTGCCCT 20

RESULT 2
 ID ADA20892 standard; DNA; 20 BP.
 AC ADA20892;
 XX 20-NOV-2003 (first entry)
 DE Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:65.
 KW BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
 KW anticonvulsant; ophthalmological; antidiabetic; virucide;
 KW antisense therapy; BAX antagonist; BAX inhibitor;
 KW familial amyotrophic lateral sclerosis; Alzheimer's disease;
 KW parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;
 KW diabetes-associated ocular disorder; scrapie infection;
 KW aberrant apoptosis; human; phosphorothioate; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages, and all cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
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 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 PN WO2003008543-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 13-JUL-2002; 2002WO-US022417.
 XX
 PR 17-JUL-2001; 2001US-00908147.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Zhang H, Watt AT;
 XX
 DR WPI; 2003-239321/23.
 XX
 XX New antisense compounds, useful for modulating the expression of BCL2-
 PT associated X (BAX) protein or for treating a disease or condition
 PT associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
 PT or Alzheimer's disease.
 XX
 PS Claim 3; Page 86; 139pp; English.
 XX
 CC The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
 CC protein, where the compound specifically hybridises with the nucleic acid
 CC molecule encoding BAX protein and inhibits the expression of BAX protein.
 CC The compound specifically hybridises with at least 8-nucleobase portion
 CC of an active site on a nucleic acid molecule encoding BAX protein. Also
 CC described: (1) a composition comprising (I) and a pharmaceutical carrier
 CC or diluent; (2) inhibiting the expression of BAX protein in cells or
 CC tissues comprising contacting the cells or tissues with (I); and (3)
 CC treating an animal having a disease or condition associated with BAX
 CC protein comprising administering to the animal (I) so that expression of

CC BAX protein is inhibited. (I) has neurotropic, neuroprotective,
 CC antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
 CC virucide activities, and can be used in antisense therapy, and as a BAX
 CC antagonist. The antisense compounds (I) are useful for modulating the
 CC expression of BAX protein, and for treating a disease or condition
 CC associated with BAX protein, e.g. familial amyotrophic lateral
 CC sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
 CC cartilage-hair hyperplasia, diabetes-associated ocular disorders or
 CC scrapie infection, or a condition that arises from aberrant apoptosis.
 CC The compounds are useful as research reagents and in diagnostics. The
 CC present sequence represents a human BAX chimeric phosphorothioate
 CC oligonucleotide, which is used in an example from the present invention.
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 90.0%; Score 18; DB 8; Length 20;
 Score over Length 90.0%;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCCCCAGTTGAAGTTGCC 18
 Db 3 GCCCCAGTTGAAGTTGCC 20

RESULT 3
 ADA20832
 ID ADA20832 standard; DNA; 18 BP.
 XX ADA20832;
 AC ADA20832;
 XX 20-NOV-2003 (first entry)
 DT Human BCL2-associated X protein reverse PCR primer SEQ ID NO:5.
 XX
 DE BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
 XX anticonvulsant; ophthalmological; antidiabetic; virucide;
 KW antisense therapy; BAX antagonist; BAX inhibitor;
 KW familial amyotrophic lateral sclerosis; Alzheimer's disease;
 KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;
 KW diabetes-associated ocular disorder; scrapie infection;
 KW aberrant apoptosis; human; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003008543-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 13-JUL-2002; 2002WO-US022417.
 XX
 PR 17-JUL-2001; 2001US-00908147.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Zhang H, Watt AT;
 XX
 DR WPI; 2003-239321/23.
 XX
 XX New antisense compounds, useful for modulating the expression of BCL2-
 PT associated X (BAX) protein or for treating a disease or condition
 PT associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
 PT or Alzheimer's disease.
 XX
 PS Example 13; Page 82; 139pp; English.
 XX
 CC The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
 CC protein, where the compound specifically hybridises with the nucleic acid
 CC molecule encoding BAX protein and inhibits the expression of BAX protein.
 CC The compound specifically hybridises with at least 8-nucleobase portion
 CC of an active site on a nucleic acid molecule encoding BAX protein. Also
 CC described: (1) a composition comprising (I) and a pharmaceutical carrier
 CC or diluent; (2) inhibiting the expression of BAX protein in cells or
 CC tissues comprising contacting the cells or tissues with (I); and (3)
 CC treating an animal having a disease or condition associated with BAX
 CC protein comprising administering to the animal (I) so that expression of

described: (1) a composition comprising (I) and a pharmaceutical carrier or diluent; (2) inhibiting the expression of BAX protein in cells or tissues comprising contacting the cells or tissues with (I); and (3) treating an animal having a disease or condition associated with BAX protein comprising administering to the animal (I) so that expression of BAX protein is inhibited. (I) has neurotropic, neuroprotective, antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and virucide activities, and can be used in antineoplastic, antidiabetic and antagonist. The antisense compounds (I) are useful for modulating the expression of BAX protein, and for treating a disease or condition associated with BAX protein, e.g. familial amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease, cartilage-hair hyperplasia, diabetes-associated ocular disorders or scrapie infection, or a condition that arises from aberrant apoptosis. The compounds are useful as research reagents and in diagnostics. The present sequence represents a PCR primer for the human BAX protein, which is used in an example from the present invention.

Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 8; Length 18;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAGTT 15
| | | | | | | | | | | | | | | | | |
Db 4 GCCCAGTTGAAGTT 18

RESULT 4
ABH71796/c
ID ABH71796 standard; DNA; 12 BP.
XX
AC ABH71796;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 271773 for detecting SNP TSC0002613.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 271773; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 5; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
| | | | | | | | | | | | | | | | | |
Db 10 AGTTGAAGTT 1

RESULT 5
ABH74771/c
ID ABH74771 standard; DNA; 12 BP.
XX
AC ABH74771;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 274756 for detecting SNP TSC0003668.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 274756; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 5; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 310208; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 5; Length 12;
 Score over Length 83.3%;
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GTTGAAGTTG 16
 Db 1 GTTGAAGTTG 10
 RESULT 9
 ABI55838/c
 ID ABI55838 standard; DNA; 12 BP.
 XX
 AC ABI55838;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 DE Oligonucleotide primer SEQ ID NO 355811 for detecting SNP TSC0049826.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 XX 18-OCT-2001.
 PD
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 355811; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 5; Length 12;
 Score over Length 83.3%;
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 AGTGAAGTT 15
 Db 10 AGTGAAGTT 1
 RESULT 10
 ADA20946
 ID ADA20946 standard; DNA; 20 BP.
 XX
 AC ADA20946;
 XX
 DT 20-NOV-2003 (first entry)
 DE
 DE Mouse BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:119.
 XX
 KW BCL2-associated X; BAX; nootropic; neuroprotective; antiparkinsonian;
 KW anticonvulsant; ophthalmological; antidiabetic; virucide;
 KW antisense therapy; BAX antagonist; BAX inhibitor;
 KW familial amyotrophic lateral sclerosis; Alzheimer's disease;
 KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;
 KW diabetes-associated ocular disorder; scrapie infection;
 KW aberrant apoptosis; mouse; phosphorothioate; ss.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 XX Location/Qualifiers
 FH modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages, and all cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 XX
 PN WO2003008543-A2.
 XX
 XX 30-JAN-2003.
 PD
 PF 13-JUL-2002; 2002WO-US022417.
 XX

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PR 17-JUL-2001; 2001US-00908147.
XX (ISIS-) ISIS PHARM INC.
XX Zhang H, Watt AT;
XX WPI; 2003-239321/23.
XX New antisense compounds, useful for modulating the expression of BCL2-
PT associated X (BAX) protein or for treating a disease or condition
PT associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
PT or Alzheimer's disease.
XX Claim 3; Page 93; 139pp; English.
XX The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
CC protein, where the compound specifically hybridizes with the nucleic acid
CC molecule encoding BAX protein and inhibits the expression of BAX protein.
CC The compound specifically hybridizes with at least 8-nucleobase portion
CC of an active site on a nucleic acid molecule encoding BAX protein. Also
CC described: (1) a composition comprising (I) and a pharmaceutical carrier
CC or diluent; (2) inhibiting the expression of BAX protein in cells or
CC tissues comprising contacting the cells or tissues with (I); and (3)
CC treating an animal having a disease or condition associated with BAX
CC protein comprising administering to the animal (I) so that expression of
CC BAX protein is inhibited. (I) has neurotropic, neuroprotective,
CC antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
CC virucide activities, and can be used in antisense therapy, and as a BAX
CC antagonist. The antisense compounds (I) are useful for modulating the
CC expression of BAX protein, and for treating a disease or condition
CC associated with BAX protein, e.g. familial amyotrophic lateral
CC sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
CC cartilage-hair hyperplasia, diabetes-associated ocular disorders or
CC scrapie infection, or a condition that arises from aberrant apoptosis.
CC The compounds are useful as research reagents and in diagnostics. The
CC present sequence represents a mouse BAX chimeric phosphorothioate
CC oligonucleotide, which is used in an example from the present invention.
XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
SQ Query Match 82.0%; Score 16.4; DB 8; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTGGCGT 20
Db 1 CCCAGTTGAAGTGGCAT 18

RESULT 11
AAQ83299
ID AAQ83299 standard; DNA; 14 BP.
XX AAQ83299;
AC AAQ83299;
XX 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
DE c-jun antisense oligonucleotide.
XX c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
KW phosphorothioate; ss.
OS Synthetic.
XX WO9502051-A2.
PN 19-JAN-1995.
XX 06-JUL-1994; 94WO-EP002218.
XX

PR 10-JUL-1993; 93EP-00111059.
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;
XX WPI; 1995-066896/09.
XX Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
PT treating neuronal injury, degeneration, cell death and/or neoplasms.
XX Claim 2; Page 30; 86pp; English.
XX Antisense nucleic acid hybridizing with an area of the mRNA and/or DNA
CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a
CC causal role in neuronal injury, degeneration, cell death and/or
CC neoplasms, can be used to prevent and treat such conditions. c-jun
CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
CC antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
CC fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
CC Preferably the antisense sequences are phosphorothioate oligonucleotides
CC since these are not destroyed as fast by endogenous factors as naturally
CC occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 14 BP; 2 A; 1 C; 6 G; 5 T; 0 U; 0 Other;
SQ Query Match 57.0%; Score 11.4; DB 2; Length 14;
Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCGG 19
Db 2 GTTGAAGTTGCTG 14

RESULT 12
ABX13068
ID ABX13068 standard; DNA; 20 BP.
XX ABX13068;
AC ABX13068;
XX 29-MAY-2003 (first entry)
DT Human bax PCR primer #2.
DE Human; insulin-like growth factor binding protein 5; IGFBP-5; primer; ss;
KW cytostatic; apoptosis; cancer; breast; prostate; ovary; lung; colon; PCR;
KW bax.
XX Homo sapiens.
XX WO2003006029-A1.
PN 23-JAN-2003.
XX 15-JUL-2002; 2002WO-AU000936.
XX 13-JUL-2001; 2001AU-00006331.
XX (UNSY ) UNIV SYDNEY.
XX Baxter RC, Butt AJ;
XX WPI; 2003-221646/21.
XX Inducing apoptosis in cancer cell, useful for treating cancer, e.g.
PT breast or prostate cancer comprises increasing the expression of insulin-
PT like growth factor binding protein-5 (IGFBP-5) by the cell to an
PT apoptosis-inducing amount.
XX Example; Page 29; 65pp; English.
XX

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CC The invention relates to a method for inducing apoptosis in a cancer cell
CC comprising increasing the expression of insulin-like growth factor
CC binding protein 5 (IGFBP-5) by the cell to an apoptosis-inducing amount.
CC The invention also relates to a method of sensitizing a cancer cell to
CC stimuli that induce apoptosis by increasing the expression of IGFBP-5 by
CC the cell, a method of killing a cancer cell by sensitizing the cell to
CC stimuli that induce apoptosis and simultaneously exposing the cell to
CC apoptosis-inducing stimuli, or exposing the cell to apoptosis-inducing
CC stimuli and simultaneously or subsequently increasing the expression of
CC IGFBP-5 by the cell to an apoptosis-inducing amount. The methods are
CC useful for treating cancer, such as breast, prostate, ovarian, lung or
CC colon cancer, by inducing apoptosis or killing cancer cells. This
CC sequence represents a bax PCR primer used in the method of the invention
XX
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 8; Length 20;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
|||||
Db 1 CAGTTGAAGTTGCCGT 16

RESULT 13
AED12216
ID AED12216 standard; DNA; 20 BP.

XX AC AED12216;

XX DT 01-DEC-2005 (first entry)

XX DE Bax (human) RT-PCR primer SEQ ID 16.

XX KW Drug screening; apoptosis; protein interaction; Bax; Cytostatic;
KW Neuroprotective; cancer; neurodegenerative disease; ss; RT-PCR;
KW reverse transcriptase PCR; primer.

XX OS Homo sapiens.

XX PN WO2005093082-A1.

XX PD 06-OCT-2005.

XX PF 23-MAR-2005; 2005WO-JP005247.

XX PR 26-MAR-2004; 2004JP-00093286.

XX PR 14-JUN-2004; 2004JP-00176107.

XX PA (HISM) HISAMITSU PHARM CO LTD.
XX (CHIB-) CHIBA PREFECTURE.

XX PI Nakagawara A, Ozaki T;

XX DR WPI; 2005-713863/73.

XX PT Screening compound capable of stimulating or inhibiting apoptosis,
PT involves judging compound capable of intensifying interaction between p73
PT and IKK-alpha as compound capable of stimulating or inhibiting apoptosis.

XX PS Example; SEQ ID NO 16; 79pp; Japanese.

XX CC The invention relates to screening (M1) a compound capable of stimulating
CC or inhibiting apoptosis, comprising identifying a compound capable of
CC modulating the interaction between p73 and IKK-alpha (IkappaB kinase) as
CC a compound capable of stimulating or inhibiting apoptosis. The method
CC comprise culturing a cell that expresses p73 and IKK-alpha in the
CC presence or absence of test compound, measuring an interaction between
CC p73 and IKK-alpha in each cultured cell and judging a compound as being
CC capable of stimulating or inhibiting apoptosis, when an interaction
CC between p73 and IKK-alpha in the cell cultured in the presence of test

CC compound, is stronger or weaker, in comparison to cell cultured in the
CC absence of test compound, respectively. Also included are an apoptosis
CC stimulator comprising AED12224 (human IKK-alpha, or a nucleic acid that
CC encodes human IKK-alpha) and an apoptosis inhibitor comprising human IKK-
CC alpha K44A mutant (AED12225) or human ubiquitin fusion degradation
CC protein-2a (AED12226). The method is useful for screening a compound
CC capable of stimulating or inhibiting apoptosis utilized for treating
CC cancer or neurodegenerative diseases. The present sequence is an RT-PCR
CC primer for a non-IKK mRNA (i.e. is either a control or is for an IKK
CC binding protein).

XX SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 17; Length 20;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20

Db 1 CAGTTGAAGTTGCCGT 16

RESULT 14

AEJ97326

ID AEJ97326 standard; DNA; 20 BP.

XX AC AEJ97326;

XX DT 02-NOV-2006 (first entry)

XX DE RT-PCR primer BAX reverse, SEQ ID 8.

XX KW Therapeutic; apoptosis inhibition; apoptosis stimulation; neoplasm;

XX KW cancer; neurodegenerative disease; neurological disorder; RT-PCR; primer;
ss.

XX OS Homo sapiens.

XX PN JP2006223265-A.

XX PD 31-AUG-2006.

XX PF 21-FEB-2005; 2005JP-00044554.

XX PR 21-FEB-2005; 2005JP-00044554.

XX PA (HISM) HISAMITSU PHARM CO LTD.
XX (CHIB-) CHIBA PREFECTURE.

XX PI Nakagawara A, Ozaki T;

XX DR WPI; 2006-590511/61.

XX PT Screening compound capable of promoting or suppressing apoptosis, for
PT treating cancer or neurodegenerative disease, involves determining
PT whether compound inhibits or enhances interaction of p53 and NFBD1.

XX PS Example; SEQ ID NO 8; 21pp; Japanese.

XX CC The invention relates to the screening of a compound capable of promoting
CC or suppressing apoptosis. The method comprises determining whether a
CC compound inhibits or enhances the interaction of p53 and NFBD1 (nuclear
CC factor with BRC domains protein 1), or culturing a cell expressing p53
CC and NFBD1 in the presence and in the absence of a test compound and
CC measuring the interaction of p53 and NFBD1 in a cultured cell. Further
CC disclosed is an apoptosis inhibitor with p53 binding activity having an
CC amino acid sequence as given in AEJ97331. The method is useful for
CC screening a compound that promotes or suppresses apoptosis and is useful
CC as a therapeutic agent for cancer and neurodegenerative disorders. The
CC current sequence represents an RT-PCR primer used in an exemplification
CC of the invention.

SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 19; Length 20;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CAGTTGAAGTTGCCGT 20
|||||
Db 1 CAGTTGAAGTTGCCGT 16

RESULT 15
AEK58344
ID AEK58344 standard; DNA; 20 BP.
XX AEK58344;
AC AEK58344;
XX
DT 16-NOV-2006 (first entry)
DE Interferon-related gene specific PCR primer, SEQ ID NO:21.
XX
KW screening; gene expression; hepatitis C virus infection;
KW antiinflammatory; hepatotropic; virucide; gastrointestinal disease;
KW infection; diagnostic; diagnosis; liver cirrhosis; inflammation;
KW microarray; DNA amplification; therapeutic; ss; primer; PCR; interferon.
XX
OS Homo sapiens.
XX
XX
PN WO2006085407-A1.
XX
PD 17-AUG-2006.
XX
XX 30-SEP-2005; 2005WO-IP018573.
XX
XX 09-FEB-2005; 2005JP-00033707.
XX
XX (UYN1-) UNIV NIPPON.
PA
XX
XX
PI Esumi M, Takayama T;
XX
XX
DR WPI; 2006-680124/70.
XX
XX
PT Screening gene whose expression is increased in high/low hepatitis C
PT virus (HCV) tissue, involves selecting gene based on its expression level
PT in low and high virus group tissues being selected based on HCV 18SrRNA
PT analysis.
XX
PS Example 1; SEQ ID NO 21; 75pp; Japanese.
XX

The new invention relates to screening a gene whose expression is
CC increased in high hepatitis C virus (HCV) group tissue or low HCV group
CC tissue. The method involves selecting liver tissue whose value is
CC obtained by dividing copy number of HCV per 50 ng of liver tissue-derived
CC cDNA by the value of 18S-RNA is not more than 300 units as low virus
CC group tissue and not more than 30000 units as high virus group tissue,
CC measuring gene expression level in tissues, and selecting gene whose
CC expression is increased in high/low virus group tissue more than low/high
CC virus group tissue. Also described is a diagnostic of diseases relevant
CC to viral load, comprising (a) gene (e.g. OASL, EHF, CXCL6, IRS2, MAP1B
CC and CXCL10) with a sequence of one of SEQ ID No. 54-131, where the
CC expression of the gene enhances in high virus group, (b) gene (e.g.
CC FLJ4615, 28S rRNA, ENCL1, RAP81, BAGE and PSMA8) comprising a sequence of
CC one of SEQ ID No. 132-170, where the expression of the gene enhances in
CC low virus group, (c) one of gene (e.g. HLA-DQA1, TMPRSS2, SPEC2, SNA12,
CC IF144, LEPR and FBNP1) of CHH gene cluster comprising a sequence of SEQ
CC ID No. 171-237, where the expression of the gene enhances in high virus
CC group of chronic hepatitis, (d) one of gene (e.g. FLJ46154, KCNN2, CRP,
CC LOC334345 and HMG42) of CHL gene cluster comprising a sequence of SEQ ID
CC No. 238-258, where the expression of the gene enhances in low virus group
CC of chronic hepatitis, (e) one of gene (e.g. SDS, GIP2, KLF6, ZDHHC11,
CC GAD645D, MX1 and BCL3) of LCH gene cluster comprising a sequence of one
CC of SEQ ID No. 259-285, where the expression of the gene enhances in high

CC virus group of liver cirrhosis, or (f) one of gene (e.g. MND4, CLCSF12,
CC SLC8A1, PST, API2, LARS and TBC1D1) of LCU gene cluster comprising a
CC sequence of one of SEQ ID No. 286-302, where the expression of the gene
CC enhances in low virus group of liver cirrhosis. The measurement of
CC expression is carried out using microarray and/or real-time PCR. The
CC method is useful for screening a gene whose expression is increased in a
CC high virus group tissue containing a large amount of HCV or in a low
CC virus group tissue containing small amount of HCV, for development of
CC therapeutic agent of HCV. This sequence is a primer for PCR amplification
CC of an interferon-related gene, useful in the new method of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 19; Length 20;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CAGTTGAAGTTGCCGT 20
|||||
Db 1 CAGTTGAAGTTGCCGT 16

RESULT 16
AAK75721/c
ID AAK75721 standard; RNA; 15 BP.
XX
AC AAK75721;
XX
DT 28-JUL-1999 (first entry)
DE Human fit-1 and KDR hammerhead ribozyme target site #55.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
PD 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-000584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Example 9; Page 191; 218pp; English.
XX

The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAK75721 to AAK75752 represent specific examples
CC of nucleic acid molecules from the present invention

```
XX SQ Sequence 15 BP; 3 A; 3 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 60.0%; Score 12; DB 2; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 17
ABF87034
ID ABF87034 standard; DNA; 13 BP.
XX AC ABF87034;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 187031 for detecting SNP TSC0046102.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PN WO200177384-A2.
XX DR 18-OCT-2001.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 187031; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 5; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 4.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAAGTTGC 12

RESULT 18
ABF87035/c
ID ABF87035 standard; DNA; 13 BP.
XX AC ABF87035;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 187032 for detecting SNP TSC0046102.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PN WO200177384-A2.
XX DR 18-OCT-2001.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 187032; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 5; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 4.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 13 AGTTGAAGTTGC 2

RESULT 19
ABI37784
ID ABI37784 standard; DNA; 12 BP.
XX AC ABI37784;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 337757 for detecting SNP TSC0004732.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 337757; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
Db 1 AGTGAAGTTG 11
RESULT 20
ABI45117/c
ID ABI45117 standard; DNA; 12 BP.
XX ABI45117;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 345090 for detecting SNP TSC0043868.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 345090; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
Db 11 AGTTGAGTTG 11
RESULT 21
ABH82576/c
ID ABH82576 standard; DNA; 12 BP.
XX ABH82576;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 282569 for detecting SNP TSC0010870.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 282569; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 12 AGTTGAGTTG 2
|||||

RESULT 22
ABI29461
ID ABI29461 standard; DNA; 12 BP.
XX
AC ABI29461;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329434 for detecting SNP TSC0034943.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 329434; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 1 AGTAGAAGTTG 11
|||||

RESULT 23
ABI05273
ID ABI05273 standard; DNA; 12 BP.
XX
AC ABI05273;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 305246 for detecting SNP TSC0021354.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 305246; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 2 AGTTGAGTTG 12
|||||


```
PR 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PS Claim 1; SEQ ID NO 281972; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
DB 11 AGTTGAGTTG 1
RESULT 27
AB139385/C
ID AB139385 standard; DNA; 12 BP.
XX
AC AB139385;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 339358 for detecting SNP TSC0040959.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 281972; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
DB 11 AGTTGAGTTG 1
RESULT 28
ABH80268
ID ABH80268 standard; DNA; 12 BP.
XX
AC ABH80268;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 280261 for detecting SNP TSC0008409.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 280261; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
```

```

CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 12;
  Score over Length 78.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db ||||| |||
1 AGTTGAAGTTG 11

RESULT 29
AB114375
ID AB114375 standard; DNA; 12 BP.
XX AC AB114375;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 314348 for detecting SNP TSC0026294.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 314348; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 12;
  Score over Length 78.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db ||||| |||
1 AGTTGAAGTTG 11

RESULT 31
AEM30648
ID AEM30648 standard; RNA; 12 BP.
XX AC AEM30648;
XX DT 08-MAR-2007 (first entry)
XX OS E. coli rRNA sequence #54.

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Db 2 AGTTAAAGTTG 12

RESULT 30
ABH75142/c
ID ABH75142 standard; DNA; 12 BP.
XX AC ABH75142;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 275133 for detecting SNP TSC0003795.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 275133; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 12;
  Score over Length 78.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db ||||| |||
12 AGTTGAAGTTG 2

RESULT 31
AEM30648
ID AEM30648 standard; RNA; 12 BP.
XX AC AEM30648;
XX DT 08-MAR-2007 (first entry)
XX OS E. coli rRNA sequence #54.

```

```
XX RNA detection; fluorescence; protein production; bacterial infection;
KW Escherichia coli infection; Pseudomonas aeruginosa infection; ss.
XX Escherichia coli.
XX WO2006122277-A2.
XX 16-NOV-2006.
XX 11-MAY-2006; 2006WO-US018320.
XX 11-MAY-2005; 2005US-0680138P.
XX 25-AUG-2005; 2005US-0711492P.
XX (UYWA-) UNIV WAYNE STATE.
XX Cunningham PR;
XX WPI; 2007-132103/13.
XX New nucleic acids that are conserved and variable regions of Escherichia
PT coli 16S rRNA, useful as targets for pharmaceuticals that are
PT taxonomically specific and/or refractory for developing drug resistance.
XX Example; Fig 5.10; 232pp; English.
XX The invention relates to a nucleic acid represented by a specific
CC formula. The invention also relates to a method of identifying an agent
CC that binds to a nucleic acid, a method of identifying an inhibitor of
CC protein synthesis, a compound obtained by the method and a method of
CC administering a compound to a patient in need. Identifying an agent,
CC which binds to a nucleic acid of the invention comprises measuring the
CC fluorescence of the nucleic acid, thus establishing a first fluorescence
CC reading, contacting a test compound with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a second fluorescence
CC reading, determining the difference between the first fluorescence
CC reading and the second fluorescence reading and selecting the compound
CC where the difference between the first fluorescence reading and the
CC second fluorescence reading is non-zero, thus identifying the agent. It
CC further comprises modifying the agent identified, thus forming a modified
CC agent, contacting the modified agent with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a modified second
CC fluorescence reading, determining the difference between the first
CC fluorescence reading and the modified second fluorescence reading and
CC selecting the compound where the difference between the first
CC fluorescence reading and the second modified fluorescence reading is non-
CC zero, thus identifying a modified agent. Assaying the inhibitory
CC properties of the agent comprises detecting protein synthesis or
CC determining the inhibitor constant for inhibiting mRNA translation. The
CC nucleic acids are conserved and can be used as targets for
CC pharmaceuticals that are taxonomically specific, refractory to the
CC development of drug resistance or both. They can also be used for
CC identifying an inhibitor of protein synthesis. The compound can be
CC administered to a patient having a microbial infection, preferably a
CC bacterial infection, e.g. E. coli or Pseudomonas aeruginosa infection.
XX This sequence represents E. coli rRNA used in the scope of the invention.
XX Sequence 12 BP; 3 A; 1 C; 4 G; 0 T; 4 U; 0 Other;
XX Query Match 47.0%; Score 9.4; DB 22; Length 12;
XX Score over Length 78.3%;
XX Best Local Similarity 63.6%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX 6 AGTTGAAGTTG 16
XX 2 AGUUGAAGCUG 12
XX
XX RESULT 32
XX AEM30671
XX ID AEM30671 standard; RNA; 12 BP.
```

```
XX AEM30671;
XX 08-MAR-2007 (first entry)
XX E. coli rRNA sequence #77.
XX RNA detection; fluorescence; protein production; bacterial infection;
KW Escherichia coli infection; Pseudomonas aeruginosa infection; ss.
XX Escherichia coli.
XX WO2006122277-A2.
XX 16-NOV-2006.
XX 11-MAY-2006; 2006WO-US018320.
XX 11-MAY-2005; 2005US-0680138P.
XX 25-AUG-2005; 2005US-0711492P.
XX (UYWA-) UNIV WAYNE STATE.
XX Cunningham PR;
XX WPI; 2007-132103/13.
XX New nucleic acids that are conserved and variable regions of Escherichia
PT coli 16S rRNA, useful as targets for pharmaceuticals that are
PT taxonomically specific and/or refractory for developing drug resistance.
XX Example; Fig 5.10; 232pp; English.
XX The invention relates to a nucleic acid represented by a specific
CC formula. The invention also relates to a method of identifying an agent
CC that binds to a nucleic acid, a method of identifying an inhibitor of
CC protein synthesis, a compound obtained by the method and a method of
CC administering a compound to a patient in need. Identifying an agent,
CC which binds to a nucleic acid of the invention comprises measuring the
CC fluorescence of the nucleic acid, thus establishing a first fluorescence
CC reading, contacting a test compound with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a second fluorescence
CC reading, determining the difference between the first fluorescence
CC reading and the second fluorescence reading and selecting the compound
CC where the difference between the first fluorescence reading and the
CC second fluorescence reading is non-zero, thus identifying the agent. It
CC further comprises modifying the agent identified, thus forming a modified
CC agent, contacting the modified agent with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a modified second
CC fluorescence reading, determining the difference between the first
CC fluorescence reading and the modified second fluorescence reading and
CC selecting the compound where the difference between the first
CC fluorescence reading and the second modified fluorescence reading is non-
CC zero, thus identifying a modified agent. Assaying the inhibitory
CC properties of the agent comprises detecting protein synthesis or
CC determining the inhibitor constant for inhibiting mRNA translation. The
CC nucleic acids are conserved and can be used as targets for
CC pharmaceuticals that are taxonomically specific, refractory to the
CC development of drug resistance or both. They can also be used for
CC identifying an inhibitor of protein synthesis. The compound can be
CC administered to a patient having a microbial infection, preferably a
CC bacterial infection, e.g. E. coli or Pseudomonas aeruginosa infection.
XX This sequence represents E. coli rRNA used in the scope of the invention.
XX Sequence 12 BP; 3 A; 1 C; 4 G; 0 T; 4 U; 0 Other;
XX Query Match 47.0%; Score 9.4; DB 22; Length 12;
XX Score over Length 78.3%;
XX Best Local Similarity 63.6%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX 6 AGTTGAAGTTG 16
XX ||:|||:::|
XX
```

```
Db 2 AGCUGAAGUUG 12

RESULT 33
ABV73748/c
ID ABV73748 standard; DNA; 22 BP.
XX
AC ABV73748;
XX
DT 30-DEC-2002 (first entry)
XX
DE Human Bax sense PCR primer.
XX
KW Cell adhesion; apoptosis; peritoneum; Bax; human; vulnery; cytostatic;
KW antinflammatory; antiinfertility; gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200272130-A1.
XX
PD 19-SEP-2002.
XX
PF 11-MAR-2002; 2002WO-US007119.
XX
PR 13-MAR-2001; 2001US-0275349P.
XX
PA (UYWA-) UNIV WAYNE STATE.
XX
PI Diamond MP, Saed GM;
XX
DR WPI; 2002-740784/80.
XX
PT Preventing or remedying surgical adhesion, useful for preventing
PT infection, pain or inflammation after surgery or during wound healing, by
PT modulating apoptosis in peritoneal cells in a subject using Bax agonists
PT or Bcl-2 antagonists.
XX
PS Example 1; Page 16; 24pp; English.
XX
CC The present sequence is a sense primer for the human Bax gene coding
CC region. Use with the antisense primer given in ABV73749 gives a 135 bp
CC PCR product. Multiplex RT-PCR was used for the simultaneous amplification
CC of Bcl-2, Bax and beta-actin mRNAs in peritoneal and adhesion fibroblasts
CC in response to hypoxia. The results showed that adhesion fibroblasts have
CC almost double the Bcl-2/Bax mRNA ratio as peritoneal fibroblasts. Hypoxia
CC resulted in a 25% decrease in the Bcl-2/Bax ratio for normal peritoneum
CC fibroblasts, indicating an increase in apoptosis. Hypoxia also resulted
CC in a 33% increase in the Bcl-2/Bax ratio for adhesion fibroblasts,
CC indicating a decrease in apoptosis. The Bcl-2/Bax ratio can determine
CC whether cells die by apoptosis, or be protected from it. The higher the
CC ratio, the lower the apoptosis rate. The invention provides a method for
CC the prevention or remediation of surgical adhesion by modulating
CC apoptosis in peritoneal, especially fibroblast, cells. The rate of
CC apoptosis is increased using a therapeutic formulation comprising Bax,
CC Bax enhancer (e.g. p53), Bax agonist, Bcl-2 inhibitor or Bcl-2
CC antagonist. A gene therapy method which introduces the p53 or Bax gene
CC into the fibroblast cells may be used. Determination of the Bcl-2/Bax
CC ratio can be used to determine whether a human subject, or an organ or
CC tissue site, is predisposed to develop adhesions during or following
CC surgery. The method is particularly useful for preventing the development
CC of post-operative adhesions in of patients following surgery, e.g.
CC ovarian cystectomy, laparoscopic or open cholecystectomy, colectomy,
CC splenectomy, kidney transplantation, or caesarean section. It is also
CC useful in preventing or eliminating cell proliferation or migration,
CC infection or inflammation during the wound healing process, in preventing
CC bowel obstruction, pain and infertility, in preventing pannus formation,
CC or for treating inflammation
XX
SQ Sequence 22 BP; 5 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 7; Length 22;
Score over Length 77.3%;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTCCCGT 20
DB 22 CCAGTTGAAGTCCCGT 6

RESULT 34
AAZ21922/c
ID AAZ21922 standard; DNA; 13 BP.
XX
AC AAZ21922;
XX
DT 24-NOV-1999 (first entry)
XX
DE Fragment of the VDJ joint of a heterologous antibody.
XX
KW Transgenic animal; heterologous antibody; hybridoma; B cell;
KW transgenic mouse; human heavy chain transgene; digoxin;
KW human light chain transgene; immortalized cell; immunoglobulin;
KW Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS Synthetic.
XX
PN WO9945962-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005535.
XX
PR 13-MAR-1998; 98US-00042353.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Lonberg N, Fishwild DM, Ball WJ;
XX
DR WPI; 1999-551219/46.
XX
PT Novel transgenic non-human animals used to produce heterologous
PT antibodies.
XX
PS Example 12; Page 177; 484pp; English.
XX
CC The specification describes transgenic animals that are capable of
CC producing a heterologous antibody. The antibodies are isolated from a
CC hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC having a genome comprising a human heavy chain transgene and a human
CC light chain transgene. The B cells are fused to immortalized cells
CC suitable for generating a hybridoma, which produces a detectable amount
CC of an immunoglobulin that specifically binds digoxin or Shinga-like
CC toxin. B cells from transgenic animals can be used to generate hybridomas
CC expressing monoclonal high affinity human sequence antibodies. Antibodies
CC produced from the transgenic animals of the invention can be used to
CC treat human diseases, e.g. autoimmune diseases, cancer, infectious
CC disease, transplant rejection, blood disorders such as coagulation
CC disorders and other diseases. AAZ21902-54 represent fragments of the VDJ
CC joint from 30 clones of the heterologous antibody of the invention
XX
SQ Sequence 13 BP; 2 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 2; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTTGA 11
DB 10 CCCAGTTGA 1

RESULT 35
ABF31261/c
```

ID XX ABEF31261 standard; DNA; 13 BP.
AC XX ABEF31261;
XX XX
DT XX 21-FEB-2002 (first entry)
XX XX
DE XX Oligonucleotide SEQ ID NO 131258 for detecting SNP TSC0032754.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
OS Homo sapiens.
XX XX
PN WO200177384-A2.
XX XX
PD 18-OCT-2001.
XX XX
PF 06-APR-2001; 2001WO-IB000713.
XX XX
PR 07-APR-2000; 2000DE-01019173.
XX XX
PA (EPIG-) EPIGENOMICS AG.
XX XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 131258; 29pp + Sequence Listing; German.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 131258; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB099989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 7 GTTGAAGTTG 16
Db 13 GTTGAAGTTG 4
XX
RESULT 36
ABF71654
ID ABF71654 standard; DNA; 13 BP.
XX
AC ABEF71654;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 171651 for detecting SNP TSC0042787.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX

OS Homo sapiens.
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 171651; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB099989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11
XX
RESULT 37
ABF50115/c
ID ABF50115 standard; DNA; 13 BP.
XX
AC ABEF50115;
XX
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 150112 for detecting SNP TSC0037893.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX

PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 150112; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1
XX
XX RESULT 38
XX ABF07779/c
ID ABF07779 standard; DNA; 13 BP.
XX
XX AC ABF07779;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 107776 for detecting SNP TSC0026982.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 107776; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1
XX
XX RESULT 39
XX ABC65593/c
ID ABC65593 standard; DNA; 13 BP.
XX
XX AC ABC65593;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 65610 for detecting SNP TSC0017271.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 65610; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
SQ

Query Match	50.0%;	Score 10;	DB 5;	Length 13;	
Score over Length	76.9%;				
Best Local Similarity	100.0%;	Pred. No. 7.3e+05;			
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	6 AGTTGAAGTT 15				
Db	10 AGTTGAAGTT 1				
RESULT 40					
ABF07778					
ID	ABF07778 standard; DNA; 13 BP.				
XX	AC AC				
XX	ABF07778;				
XX					
DT	21-FEB-2002 (first entry)				
XX					
DE	Oligonucleotide SEQ ID NO 107775 for detecting SNP TSC0026982.				
XX					
KW	SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;				
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;				
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200177384-A2..				
XX					
PD	18-OCT-2001.				
XX					
PF	06-APR-2001; 2001WO-IB000713.				
XX					
PR	07-APR-2000; 2000DE-01019173.				
XX					
PA	(EPIG-) EPIGENOMICS AG.				
XX					
PI	Olek A, Piepenbrock C, Berlin K;				
XX					
DR	WPI; 2001-657177/75.				
XX					
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is				
PT	designed to detect single-nucleotide polymorphisms and cytosine				
PT	methylation status.				
XX					
PS	Claim 1; SEQ ID NO 107775; 29pp + Sequence Listing; German.				
XX					
CC	This invention describes novel oligonucleotide primers or peptide nucleic				
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)				
CC	and cytosine methylation status in chemically pretreated genomic DNA. The				
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a				
CC	range of diseases including immune system, gastrointestinal, respiratory,				
CC	central nervous system, cardiovascular and metabolic disorders. The				
CC	oligomers are also used for detecting cell type differentiation. ABC00010				
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073				
CC	represent the oligomers described in the invention. NOTE: The sequence				
CC	data for this patent did not form part of the printed specification, but				
CC	was obtained in electronic format from WIPO at				
CC	ftp.wipo.int/pub/published_pct_sequences				
XX					
SQ	Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;				
Query Match	50.0%;	Score 10;	DB 5;	Length 13;	
Score over Length	76.9%;				
Best Local Similarity	100.0%;	Pred. No. 7.3e+05;			
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	6 AGTTGAAGTT 15				
Db	3 AGTTGAAGTT 12				
RESULT 41					

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 4 AGTTGAAGTT 13

RESULT 45
ABF53415/C
ID ABF53415 standard; DNA; 13 BP.
XX
AC ABF53415;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 153412 for detecting SNP TSC0038780.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
PD 06-APR-2001; 2001WO-IB000713.
XX
PF 07-APR-2000; 2000DE-01019173.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 153412; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 1 Other;
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 7.3e+05;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 12 AGTTGAAGATGY 1

RESULT 46
ABF53414
ID ABF53414 standard; DNA; 13 BP.
XX
AC ABF53414;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 153411 for detecting SNP TSC0038780.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
PD 06-APR-2001; 2001WO-IB000713.
XX
PF 07-APR-2000; 2000DE-01019173.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 153411; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 1 Other;
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 7.3e+05;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 2 AGTTGAAGATGY 13

```

RESULT 47
ABF31260
ID ABF31260 standard; DNA; 13 BP.
XX
AC ABF31260;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 131257 for detecting SNP TSC0032754.
XX
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 150111; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
DB 1 GTTGAAGTTG 10
XX
RESULT 48
ABF50114
ID ABF50114 standard; DNA; 13 BP.
XX
AC ABF50114;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 150111 for detecting SNP TSC0037893.
XX
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW

```

```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 150111; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 4 AGTTGAAGTT 13
XX
RESULT 49
AEC04526
ID AEC04526 standard; cDNA; 13 BP.
XX
AC AEC04526;
XX
DT 20-OCT-2005 (first entry)
XX
DE Human breast cancer marker cDNA SEQ ID NO 704.
XX
DE Cytostatic; Gene therapy; diagnosis; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; ss; tumor marker.
XX
OS Homo sapiens.
XX
PN WO2005072050-A2.
XX
PD 11-AUG-2005.
XX
PF 27-JAN-2005; 2005WO-IB000433.
XX
PR 27-JAN-2004; 2004US-0539128P.
XX
PR 27-JAN-2004; 2004US-0539129P.
XX
PR 22-OCT-2004; 2004US-0620656P.

```


CC detecting lung cancer cells with the biomarker; (10) selecting a therapy
CC for lung cancer, which comprises detecting lung cancer cells with the
CC biomarker and selecting a therapy according to the detection; and (11) a
CC display library comprising several display vehicles, such as phages,
CC viruses or bacteria. The isolated polynucleotide is useful in detecting
CC lung cancer, in monitoring disease progression or treatment efficacy or
CC relapse of lung cancer or in selecting a therapy for lung cancer. The
CC invention provides novel markers for lung cancer that are both sensitive
CC and accurate, something which is not currently provided in the prior art.
CC The present sequence is used in the exemplification of the present
CC invention. Note - The Sequence Listing data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from the USPTO web site.

XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 19; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

DB 3 GTTGAAGTTG 12

RESULT 51

AGI70514
ID AGI70514 standard; DNA; 13 BP.

XX AC AGI70514;

XX DT 04-OCT-2007 (first entry)

XX DE Human T1628_PEA_1_node_32 SEQ ID NO: 809.

XX diagnostic; lung tumor; cancer; neoplasm; cytostatic;
KW respiratory disease; small-cell lung cancer; non-small cell lung cancer;
KW adenocarcinoma; squamous cell carcinoma; large cell carcinoma; ds.
XX
XX Homo sapiens.

XX WO2006131783-A2.

XX PD 14-DEC-2006.

XX PF 27-JAN-2005; 2005WO-IB004037.

XX PR 27-JAN-2004; 2004US-0539128P.

XX PR 27-JAN-2004; 2004US-0539129P.

XX PR 22-JUL-2004; 2004US-0589815P.

XX PR 07-SEP-2004; 2004US-0607307P.

XX PR 22-OCT-2004; 2004US-0620656P.

XX PR 22-OCT-2004; 2004US-0620677P.

XX PR 22-OCT-2004; 2004US-0620853P.

XX PR 22-OCT-2004; 2004US-0620868P.

XX PR 22-OCT-2004; 2004US-0620874P.

XX PR 22-OCT-2004; 2004US-0620916P.

XX PR 22-OCT-2004; 2004US-0620917P.

XX PR 22-OCT-2004; 2004US-0620918P.

XX PR 22-OCT-2004; 2004US-0620924P.

XX PR 22-OCT-2004; 2004US-0620974P.

XX PR 22-OCT-2004; 2004US-0620975P.

XX PR 22-OCT-2004; 2004US-0621004P.

PR 17-NOV-2004; 2004US-0628167P.

PR 17-NOV-2004; 2004US-0628178P.

PR 17-NOV-2004; 2004US-0628189P.

PR 17-NOV-2004; 2004US-0628251P.

PR 08-DEC-2004; 2004US-0634075P.

PR 27-JAN-2005; 2005US-00051720.

XX (COMP-) COMPUGEN USA INC.

XX PA Pollock S, Levine Z, Novik A, Dahary D, Sorek R, Toporik A;

XX PI Sameah-Greenwald S, Sella-Tavor O, Diber A, Cojocaru GS;

XX PI Ayalon-Soffer M, Walach S, Akiva P, Keren N, Shmehesh R;

XX DR WPI; 2007-159255/16.

XX PT New isolated polynucleotide useful as a biomarker for detecting lung

XX PT cancer comprises polynucleotide having sequence of specified nucleic

XX PT acids.

XX PS Example 5; SEQ ID NO 809; 2200pp; English.

XX CC This invention describes novel polynucleotides and polypeptides used for

XX CC the diagnosis of lung cancer. The invention claims: a) an antibody

XX CC capable of specifically binding to an epitope of an amino acid sequence

XX CC of the isolated polypeptide; b) a kit which detects the overexpression of

XX CC a splice variant of the isolated polynucleotide; c) a biomarker capable

XX CC of detecting lung cancer, comprising a nucleic acid sequence of the

XX CC isolated polynucleotide or its fragment, or an amino acid sequence of the

XX CC isolated polypeptide or its fragment; d) a method of screening and

XX CC diagnosing lung cancer and monitoring disease progression, treatment

XX CC efficacy and/or relapse of lung cancer, involving detecting lung cancer

XX CC cells with the biomarker and e) selecting a therapy for lung cancer,

XX CC involving detecting lung cancer cells with the biomarker and selecting a

XX CC therapy according to the detection. The polynucleotides are novel markers

XX CC for lung cancer that are both sensitive and accurate and also they are

XX CC able to distinguish between different types of lung cancer, such as small

XX CC cell or non-small cell lung cancer (e.g. adenocarcinomas, squamous cell

XX CC and large cell carcinomas). These markers are overexpressed in lung

XX CC cancer specifically, as opposed to normal lung tissue, and thus show a

XX CC high degree of differential detection between lung cancer and non-

XX CC cancerous states. This sequence represents a polynucleotide used in the

XX CC method of the invention.

XX SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 22; Length 13;

Score over Length 76.9%;

Best Local Similarity 100.0%; Pred. No. 7.3e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

DB 3 GTTGAAGTTG 12

RESULT 52

ABI38653/C

ID ABI38653 standard; DNA; 12 BP.

XX AC ABI38653;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 338626 for detecting SNP TSC0040587.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 338626; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GTTGAAGTT 15
Db |||||
9 GTTGAAGTT 1

RESULT 53
ABI43950/c
ID ABI43950 standard; DNA; 12 BP.
XX
AC ABI43950;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 343923 for detecting SNP TSC0043299.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 343923; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GTTGAAGTT 15
Db |||||
10 GTTGAAGTT 2

RESULT 54
ABI33999
ID ABI33999 standard; DNA; 12 BP.
XX
AC ABI33999;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 333972 for detecting SNP TSC0037861.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 333972; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GTTGAAGTT 15
Db |||||
10 GTTGAAGTT 2

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
|||||
Db 2 TTGAAGTTG 10

RESULT 55
ABI69281
ID ABI69281 standard; DNA; 12 BP.
XX
AC ABI69281;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 369254 for detecting SNP TSC0057554.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.

XX WO200177384-A2.
XX PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 369254; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GTTGAAGTT 15
|||||
Db 4 GTTGAAGTT 12

RESULT 56
ABI42808
ID ABI42808 standard; DNA; 12 BP.

XX
AC ABI42808;
XX
DT 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 342781 for detecting SNP TSC0042707.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 342781; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
|||||
Db 1 TTGAAGTTG 9

RESULT 57
ABH72541
ID ABH72541 standard; DNA; 12 BP.
XX
AC ABH72541;

```
XX 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 272526 for detecting SNP TSC0002847.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 272526; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGT 14
XX
XX DB 4 AGTTGAAGT 12
XX
XX RESULT 58
XX ABH88159
XX ID ABH88159 standard; DNA; 12 BP.
XX
XX AC ABH88159;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 288152 for detecting SNP TSC0013396.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
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XX
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XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
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XX Olek A, Piepenbrock C, Berlin K;
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XX WPI; 2001-657177/75.
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XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 288152; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TTGAAGTTG 16
XX
XX DB 2 TTGAAGTTG 10
XX
XX RESULT 59
XX ABH98609
XX ID ABH98609 standard; DNA; 12 BP.
XX
XX AC ABH98609;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 298602 for detecting SNP TSC0018187.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX
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XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 298602; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
    Query Match      45.0%; Score 9; DB 5; Length 12;
    Score over Length 75.0%;
    Best Local Similarity 100.0%; Pred. No. 2.2e+06;
    Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 9 TGAAGTTGC 17
    DB 4 TGAAGTTGC 12
    RESULT 60
    ABI37700
    ID ABI37700 standard; DNA; 12 BP.
    AC ABI37700;
    XX
    DT 22-FEB-2002 (first entry)
    XX
    DE Oligonucleotide primer SEQ ID NO 337673 for detecting SNP TSC0039994.
    XX
    KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
    KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
    KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
    XX
    OS Homo sapiens.
    XX
    PN WO200177384-A2.
    XX
    PD 18-OCT-2001.
    XX
    PF 06-APR-2001; 2001WO-IB000713.
    XX
    PR 07-APR-2000; 2000DE-01019173.
    XX
    PA (EPIC-) EPIGENOMICS AG.
    XX
    PI Olek A, Piepenbrock C, Berlin K;
    XX
    DR WPI; 2001-657177/75.
    XX
    PT Set of oligonucleotides, useful for diagnosis and cell typing, is
    PT designed to detect single-nucleotide polymorphisms and cytosine
    PT methylation status.
    XX
    PS Claim 1; SEQ ID NO 337673; 29pp + Sequence Listing; German.
    XX
    CC This invention describes novel oligonucleotide primers or peptide nucleic
    CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
    CC and cytosine methylation status in chemically pretreated genomic DNA. The
    CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
    CC range of diseases including immune system, gastrointestinal, respiratory,
    CC central nervous system, cardiovascular and metabolic disorders. The
    CC oligomers are also used for detecting cell type differentiation. ABC00010
    CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
    CC represent the oligomers described in the invention. NOTE: The sequence
    CC data for this patent did not form part of the printed specification, but
    CC was obtained in electronic format from WIPO at
    CC ftp.wipo.int/pub/published_pct_sequences
    XX
    SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
    Query Match      45.0%; Score 9; DB 5; Length 12;
    Score over Length 75.0%;
    Best Local Similarity 100.0%; Pred. No. 2.2e+06;
    Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 8 TTGAAGTTG 16
    DB 2 TTGAAGTTG 10
    RESULT 61
    ABI79970
    ID ABI79970 standard; DNA; 12 BP.
    AC ABI79970;
    XX
    DT 22-FEB-2002 (first entry)
    XX
    DE Oligonucleotide primer SEQ ID NO 379943 for detecting SNP TSC0063547.
    XX
    KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
    KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
    KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
    XX
    OS Homo sapiens.
    XX
    PN WO200177384-A2.
    XX
    PD 18-OCT-2001.
    XX
    PF 06-APR-2001; 2001WO-IB000713.
    XX
    PR 07-APR-2000; 2000DE-01019173.
    XX
    PA (EPIC-) EPIGENOMICS AG.
    XX
    PI Olek A, Piepenbrock C, Berlin K;
    XX
    DR WPI; 2001-657177/75.
    XX
    PT Set of oligonucleotides, useful for diagnosis and cell typing, is
    PT designed to detect single-nucleotide polymorphisms and cytosine
    PT methylation status.
    XX
    PS Claim 1; SEQ ID NO 379943; 29pp + Sequence Listing; German.
    XX
    CC This invention describes novel oligonucleotide primers or peptide nucleic
    CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
    CC and cytosine methylation status in chemically pretreated genomic DNA. The
    CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
    CC range of diseases including immune system, gastrointestinal, respiratory,
    CC central nervous system, cardiovascular and metabolic disorders. The
    CC oligomers are also used for detecting cell type differentiation. ABC00010
    CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
    CC represent the oligomers described in the invention. NOTE: The sequence
    CC data for this patent did not form part of the printed specification, but
    CC was obtained in electronic format from WIPO at
    CC ftp.wipo.int/pub/published_pct_sequences
    XX
    SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
    Query Match      45.0%; Score 9; DB 5; Length 12;
    Score over Length 75.0%;

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Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 4 AGTTGAAGT 12

RESULT 62
ABH98752
ID ABH98752 standard; DNA; 12 BP.
XX AC ABH98752;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 298745 for detecting SNP TSC0018260.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 298745; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABT0010-ABT82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 63
ABH10039
ID ABH10039 standard; DNA; 12 BP.
XX AC ABH10039;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 319646 for detecting SNP TSC0029341.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 310012; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABT0010-ABT82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10

RESULT 64
ABH19673/c
ID ABH19673 standard; DNA; 12 BP.
XX AC ABH19673;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 319646 for detecting SNP TSC0029341.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 310012; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABT0010-ABT82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
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PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 281370; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4
RESULT 65
ABH81377/c
ID ABH81377 standard; DNA; 12 BP.
XX
AC ABH81377;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 281370 for detecting SNP TSC0009690.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
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PI Olek A, Piepenbrock C, Berlin K;
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DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 319646; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4
RESULT 66
AB165921/c
ID AB165921 standard; DNA; 12 BP.
XX
AC AB165921;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 365894 for detecting SNP TSC0055428.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 365894; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTT 15
Db 11 GTTGAAGTT 3
RESULT 66
AB165921/c
ID AB165921 standard; DNA; 12 BP.
XX
AC AB165921;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 365894 for detecting SNP TSC0055428.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
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XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 365894; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTT 15
Db 11 GTTGAAGTT 3
```

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4

RESULT 67
ABI32591/c
ID ABI32591 standard; DNA; 12 BP.
AC ABI32591;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 332564 for detecting SNP TSC0036994.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 332564; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4

RESULT 69
ABI45848/c
ID ABI45848 standard; DNA; 12 BP.

Query Match 45.0%; Score 9; DB 5; Length 12;

Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4

RESULT 68
ABH84637/c
ID ABH84637 standard; DNA; 12 BP.
XX
AC ABH84637;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 284630 for detecting SNP TSC0011911.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 284630; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 12 AGTTGAAGT 4

RESULT 69
ABI45848/c
ID ABI45848 standard; DNA; 12 BP.

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

XX ABI45848;
AC
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 345821 for detecting SNP TSC0044228.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 345821; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 7 GTTGAAGTT 15
Db |||||||
9 GTTGAAGTT 1
XX
RESULT 70
ABI08021
ID ABI08021 standard; DNA; 12 BP.
XX
AC ABI08021;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 307994 for detecting SNP TSC0022828.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.

```

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XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 307994; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 7 GTTGAAGTT 15
Db |||||||
4 GTTGAAGTT 12
XX
RESULT 71
ABI58136
ID ABI58136 standard; DNA; 12 BP.
XX
AC ABI58136;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 358109 for detecting SNP TSC0050957.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

```

```
XX DR WPI; 2001-657177/75.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
PT PT acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
PT PT and cytosine methylation status in chemically pretreated genomic DNA. The
XX PT oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX PS range of diseases including immune system, gastrointestinal, respiratory,
XX PS central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TTGAAGTTG 16
XX DB |||||||
XX 1 TTGAAGTTG 9
XX
XX RESULT 72
XX ABH99938
XX ID ABH99938 standard; DNA; 12 BP.
XX AC ABH99938;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 299931 for detecting SNP TSC0018813.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX AC
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR
XX PR SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX AC
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR
XX PR 07-APR-2000; 2000DE-01019173.
XX PS
XX PS Claim 1; SEQ ID NO 299931; 29pp + Sequence Listing; German.
XX PA
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TTGAAGTTG 16
XX DB |||||||
XX 1 TTGAAGTTG 9
XX
XX RESULT 73
XX ABI03368/c
XX ID ABI03368 standard; DNA; 12 BP.
XX AC ABI03368;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 303341 for detecting SNP TSC0020445.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX AC
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR
XX PR 07-APR-2000; 2000DE-01019173.
XX PA
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX CC
XX CC Set of oligonucleotides, useful for diagnosis and cell typing, is
XX CC designed to detect single-nucleotide polymorphisms and cytosine
XX CC methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 303341; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
```

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Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
DB 11 AGTTGAAGT 3

RESULT 74
ABI38557/c
ID ABI38557 standard; DNA; 12 BP.
XX AC
XX AB160242;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 338530 for detecting SNP TSC0005251.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 338530; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB102073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 12 TTGAAGTTG 4

RESULT 75
ABI60242/c
ID ABI60242 standard; DNA; 12 BP.
XX AC
XX AB160242;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 360215 for detecting SNP TSC0051979.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 360215; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB102073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
DB 10 AGTTGAAGT 2

RESULT 76
ABI05053
ID ABI05053 standard; DNA; 12 BP.
XX AC
XX AB105053;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 305026 for detecting SNP TSC0021217.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```


CC polypeptide (I), characterised by a molecular weight of about 112 kDa,
 CC and substantially free of other human proteins. Also described is the DNA
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
 CC treatment of a medical condition resulting from a defect in the OPAL
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
 CC and antibodies to (I) are useful in a variety of hybridisation and
 CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OPAL gene or gene product. ABK72533-ABK72593
 CC represent the human OPAL gene and intron/exon splice junctions

XX Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 6; Length 12;
 Score over Length 75.0%;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAG 13
 |||||
 DB 4 CAGTTGAAG 12

RESULT 79
 AAX34784/c
 ID AAX34784 standard; DNA; 14 BP.

AC AAX34784;
 XX
 DT 02-JUL-1999 (first entry)
 DE Neurotensin receptor sense PNA oligomer +3765-NTR1-PNA.

XX Polyamide nucleic acid; peptide nucleic acid; PNA; biological response;
 KW Gene therapy; cancer; aging; behavioral disorder; infection; autoimmune;
 KW Huntington's disease; Alzheimer's disease; brain disorder; neurotensin;
 KW ss.

OS Rattus sp.

XX WO9920643-A1.

PN 29-APR-1999.

PD 16-OCT-1998; 98WO-US021888.

PF 17-OCT-1997; 97US-00953269.

PR 30-JAN-1998; 98US-00016685.

PR 08-OCT-1998; 98US-00168519.

PR 08-OCT-1998; 98US-00168714.

PR 08-OCT-1998; 98US-00168791.

XX (MAYO-) MAYO FOUNDATION.

XX Richelson E, Tyler BM, McCormick DJ, Cusack BM, Hoshall CV;

PI Douglas CL, Jansen K;

XX WPI; 1999-302715/25.

DR Extracellular administration of nucleic acid oligomers useful for gene

PT therapy of cancers and behavioral disorders.

XX Claim 14; Page 78; 116pp; English.

XX The invention relates to a method for the treatment of a living cell by
 CC extracellular administration of a polyamide nucleic acid (PNA) oligomer
 CC to produce a sequence-specific biological response. A method is also
 CC provided for identifying mismatch PNA that generate a biological
 CC response, in an animal, different from that produced by a reference PNA.
 CC The PNA oligomers are used to manipulate and study any polypeptide in
 CC living cells, either for research (e.g. identifying polypeptide functions
 CC or measuring the relative turn-over rate of functional polypeptides) or
 CC for gene therapy of e.g. cancer, aging, behavioral disorders, infections
 CC and autoimmune diseases, typically Huntington's and Alzheimer's diseases.

CC They can cross biological barriers (making them suitable for treating
 CC brain disorders) and elicit a sequence-specific response, eliminating the
 CC need for microinjection into cells or for cell permeabilization. They may
 CC modulate polypeptide expression by both sense and antisense mechanisms
 CC (which may be used together), and using PNA with controllable degrees of
 CC mismatch allows the response to be adjusted as required

XX Sequence 14 BP; 4 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 2; Length 14;

Score over Length 74.3%;

Best Local Similarity 91.7%; Pred. No. 4.7e+05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16

||| |||||
 DB 14 CAGATGAAGTTG 3

RESULT 80

ABC61646

ID ABC61646 standard; DNA; 13 BP.

XX ABC61646;

AC 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 61663 for detecting SNP TSC0016401.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 61663; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 1 Other;

Query Match 48.0%; Score 9.6; DB 5; Length 13;

Score over Length 73.8%;

Best Local Similarity 90.0%; Pred. No. 1.1e+06;


```
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TTGAAGTTGC 17
Db 4 TTGAAGTTGY 13
RESULT 81
ABC61647/c
ID ABC61647 standard; DNA; 13 BP.
XX
AC ABC61647;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 61664 for detecting SNP TSC0016401.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 61664; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 1 Other;

Query Match 48.0%; Score 9.6; DB 5; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 1.1e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TTGAAGTTGC 17
Db 10 TTGAAGTTGY 1
RESULT 82
AAx75746/c
ID AAx75746 standard; RNA; 15 BP.
XX
AC AAx75746;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TTGAAGTTGC 17
Db 10 TTGAAGTTGY 1
RESULT 83
AAZ64449/c
ID AAZ64449 standard; RNA; 15 BP.
XX
AC AAZ64449;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 9176.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.

XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt-1 and KDR hammerhead ribozyme target site #80.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
FN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Example 9; Page 192; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 55.0%; Score 11; DB 2; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CCAGTTGAAGT 14
Db 15 CCAGTTGAAGT 5
RESULT 84
AAZ64449/c
ID AAZ64449 standard; RNA; 15 BP.
XX
AC AAZ64449;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 9176.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
```

```
XX PN WO9955847-A2.
XX PD 04-NOV-1999.
XX PP 26-APR-1999; 99WO-US009027.
XX PR 27-APR-1998; 98US-0083217P.
XX PR 18-SEP-1998; 98US-0100842P.
XX PR 25-FEB-1999; 99US-00257608.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
XX DR WPI; 2000-062023/05.
XX NR Novel ribozymes for the treatment of diseases and conditions related to
XX PT hepatitis C infection.
XX PS Claim 1; Page 92; 123pp; English.
XX SS The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX SQ Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 55.0%; Score 11; DB 3; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 84
ID AEB76210/c
XX AEB76210 standard; RNA; 15 BP.
XX AC AEB76210;
XX DT 22-SEP-2005 (first entry)
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.
KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
KW antiviral; gene therapy; substrate; ss.
XX OS Hepatitis C virus.
XX PN US2002033458-A1.
XX PD 31-JAN-2002.
XX PF 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.

(BLATT/) BLATT L.
(MCSW/) MCSWIGGEN J A.
(ROBE/) ROBERTS E.
(PAVO/) PAVO P A.
(MACE/) MACEJACK D.

Blatt L, McSwiggen JA, Roberts E, Pavo PA, Macejack D;
WPI; 2002-215899/27.

New enzymatic nucleic acid molecule, which specifically cleaves minus
strand RNA derived from hepatitis C virus, useful for modulating the
expression and/or replication of hepatitis C virus.

Example 1; Page 42; 65pp; English.

The invention relates to an enzymatic nucleic acid molecule which
specifically cleaves minus strand RNA derived from hepatitis C virus
(HCV). The binding arms of the molecule comprise ribozyme sequences. The
molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
Zinzyne motifs. Also described: (1) a pharmaceutical composition
comprising the novel enzymatic nucleic acid; (2) a mammalian cell
including the novel enzymatic nucleic acid; (3) an expression vector
comprising a nucleic acid sequence encoding at least one enzymatic
nucleic acid molecule, in a manner, which allows expression of that
molecule; (4) a mammalian cell including an expression vector of (3); (5)
methods for treating cirrhosis, liver failure or hepatocellular carcinoma
by administering to a patient the novel enzymatic nucleic acid or the
vector of (3); (6) a method of treating a patient having a condition
associated with HCV infection, by contacting cells of the patient with
the nucleic acid molecule, and further employing one or more drug
therapies; (7) a method for inhibiting HCV replication in a mammalian
cell by administering the novel enzymatic nucleic acid; and (8) a method
of cleaving a separate RNA molecule by contacting the novel enzymatic
nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
is useful for modulating the expression and/or replication of hepatitis C
virus (HCV), and for inhibiting the expression of HCV minus strand. The
nucleic acid may also be used to treat or prevent the occurrence of a
disease state in a patient. The present sequence represents an HCV
hammerhead ribozyme target substrate sequence which is used in the
exemplification of the present invention.

Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 55.0%; Score 11; DB 6; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 85
ID ABX01502/c
XX ABX01502 standard; RNA; 15 BP.
XX AC ABX01502;
XX DT 23-DEC-2002 (first entry)
XX DE Hepatitis C virus substrate #1284 for HCV hammerhead ribozyme #1284.
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX OS Hepatitis C virus.
```

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XX PN US2002082225-A1.
XX PD . 27-JUN-2002.
XX PF 23-MAR-1999; 99US-00274553.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX PT replication and are useful to treat hepatitis C virus infections and
XX PT cirrhosis, liver failure or hepatocellular carcinoma.
XX PS Claim 1; Page 58; 80pp; English.
XX CC The present invention relates to enzymatic nucleic acids which
XX CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX CC (HP) motif where the binding arms comprise sequences complementary to one
XX CC of the substrate sequences defined in the specification. The HCV
XX CC ribozymes are useful for modulating the expression and/or replication of
XX CC HCV. They can be used to treat cirrhosis, liver failure and/or
XX CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX CC a condition associated with HCV infection in conjunction with one or more
XX CC other drug therapies, particularly type I interferon, especially
XX CC interferon alpha, beta or gamma or consensus interferon. The present
XX CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX CC Some of the sequence data for this patent did not form part of the
XX CC printed specification. The complete sequence data for this patent was
XX CC obtained in electronic format directly from the USPTO web site at
XX CC seqdata.uspto.gov/patents/entry.html
XX SQ Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 55.0%; Score 11; DB 6; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 86
ABQ77353/c
ID ABQ77353 standard; DNA; 15 BP.
XX AC ABQ77353;
XX DT 08-MAY-2003 (first entry)
XX DE Receptor synthesis associated oligonucleotide probe #4.
XX KW Probe; wet chemical; photochemical; receptor synthesis; immobilisation;
XX KW polymetric receptor; array; nucleic acid chip; computer-optimisation; ss.
XX OS Synthetic.
XX PN DE10122357-A1.
XX PD 14-NOV-2002.

XX PF 09-MAY-2001; 2001DE-01022357.
XX PR 09-MAY-2001; 2001DE-01022357.
XX PA (FEBI-) FEBIT FERRARIUS BIOTECHNOLOGY GMBH.
XX PI Staehler CF, Staehler PF, Beier M, Wixmerten A, Mauritz R;
XX PI Schlaubersbach A;
XX DR WPI; 2003-240759/24.
XX PT Preparation of carrier for determining analytes, useful particularly for
XX PT making DNA chips, uses both wet chemical and photochemical techniques for
XX PT receptor synthesis.
XX PS Disclosure; Fig 11; 24pp; German.
XX CC This invention describes a novel method for the preparation of a carrier
XX CC for determination of analytes using a combination of wet chemical and
XX CC photochemical techniques for synthesis of receptors. The method comprises
XX CC (i) passing a liquid containing nucleic acid building blocks for
XX CC synthesis of a polymetric receptor over a carrier, (ii) location- and/or
XX CC time-specific immobilisation of the building blocks at predetermined
XX CC regions and (iii) repeating the procedure to synthesise the required
XX CC polymetric receptor at selected positions. The novel feature is that
XX CC polymetric repeats are synthesised using a combination of wet chemical and
XX CC photochemical stages. The carrier described in the invention is a
XX CC receptor array, particularly a nucleic acid chip (but also arrays of
XX CC proteins, peptides and saccharides), e.g. for genomic, gene expression or
XX CC proteome analysis. The method combines the advantages of both wet
XX CC chemical and photochemical techniques, allowing preparation of many
XX CC different receptors at the same site (not possible with either technique
XX CC alone). It also allows computer-optimisation of the synthesis strategy,
XX CC including use of as many wet-chemical steps as possible for optimal
XX CC quality and greater synthesis rate. ABQ77350-ABQ77354 represent
XX CC oligonucleotide probes used to illustrate the method of the invention
XX SQ Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 8; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCC 18
Db 14 TTGAAGTTGCC 4

RESULT 87
AAQ88636
ID AAQ88636 standard; DNA; 12 BP.
XX AC AAQ88636;
XX DT 03-JAN-1996 (first entry)
XX DE Human mitochondrial D-loop region DNA probe 16-12.
XX KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
XX KW D-loop region; biological chip; hybridisation fingerprint;
XX KW interrogation position; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 12
XX FT /*tag= a
XX FT /note= "3'-end of probe is covalently attached to chip
XX PN WO9511995-A1.

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PD 04-MAY-1995.
XX
XX PF 26-OCT-1994; 94WO-US012305.
XX
XX PR 26-OCT-1993; 93US-00143312.
XX
XX PR 02-AUG-1994; 94US-00284064.
XX
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
XX PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
XX DR WPI; 1995-178887/23.
XX
XX PT New arrays of oligo:nucleotide probes - used for comparing known
XX PT sequences with variants for detection of mutation(s) and sequencing.
XX
XX PS Disclosure; Page 108; 223pp; English.
XX
XX CC A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX CC fragment of human mitochondrial DNA from the D-loop region, the most
XX CC polymorphic region of human mitochondrial DNA. The chip comprised a set
XX CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
XX CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX CC x 1cm array. Each position in the sequence was represented by at least
XX CC one probe (usually 2 or more). DNA was amplified from six human donors
XX CC and then transcribed to give the 1.3kb RNA transcripts which were
XX CC fragmented and hybridised to the chip. For each individual, a unique
XX CC hybridisation fingerprint was produced on the chip; all differences could
XX CC be correlated with differences in the cloned genomic DNA sequence
XX
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
    Query Match 44.0%; Score 8.8; DB 2; Length 12;
    Score over Length 73.3%;
    Best Local Similarity 83.3%; Pred. No. 2.8e+06;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAGTTGC 17
DB 1 ATTTGAGTTGC 12

RESULT 88
AAQ88635
ID AAQ88635 standard; DNA; 12 BP.
XX
XX AC AAQ88635;
XX
XX DT 03-JAN-1996 (first entry)
XX
XX DE Human mitochondrial D-loop region DNA probe 15-12.
XX
XX KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
XX KW D-loop region; biological chip; hybridisation fingerprint;
XX KW interrogation position; ss.
XX
XX OS Synthetic.
XX
XX FH Key
XX modified_base 12
XX Location/Qualifiers
XX
XX FT /*tag= a
XX FT /note= "3'-end of probe is covalently attached to chip
XX FT surface"
XX
XX PN W09511995-A1.
XX
XX PD 04-MAY-1995.
XX
XX PF 26-OCT-1994; 94WO-US012305.
XX
XX PR 26-OCT-1993; 93US-00143312.
XX
XX PR 02-AUG-1994; 94US-00284064.
XX
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
XX PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
XX DR WPI; 1995-178887/23.
XX
XX PT New arrays of oligo:nucleotide probes - used for comparing known
XX PT sequences with variants for detection of mutation(s) and sequencing.
XX
XX PS Disclosure; Page 108; 223pp; English.
XX
XX CC A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX CC fragment of human mitochondrial DNA from the D-loop region, the most
XX CC polymorphic region of human mitochondrial DNA. The chip comprised a set
XX CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
XX CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX CC x 1cm array. Each position in the sequence was represented by at least
XX CC one probe (usually 2 or more). DNA was amplified from six human donors
XX CC and then transcribed to give the 1.3kb RNA transcripts which were
XX CC fragmented and hybridised to the chip. For each individual, a unique
XX CC hybridisation fingerprint was produced on the chip; all differences could
XX CC be correlated with differences in the cloned genomic DNA sequence
XX
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
    Query Match 44.0%; Score 8.8; DB 2; Length 12;
    Score over Length 73.3%;
    Best Local Similarity 83.3%; Pred. No. 2.8e+06;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 1 TGGAGTTGCAGT 12

RESULT 89
AAZ30061
ID AAZ30061 standard; DNA; 12 BP.
XX
XX AC AAZ30061;
XX
XX DT 26-JAN-2000 (first entry)
XX
XX DE Splice acceptor site of exon 3 of IL-1 receptor antagonist DNA.
XX
XX KW Human; interleukin-1 receptor; IL-1; antagonist; sepsis;
XX KW acute pancreatitis; endotoxin shock; cytokine induced shock;
XX KW rheumatoid arthritis; chronic inflammatory arthritis;
XX KW pancreatic cell damage; diabetes mellitus type 1;
XX KW graft versus host disease; inflammatory bowel disease; inflammation;
XX KW pulmonary disease; autoimmune disease; inflammatory disease;
XX KW antiproliferative; myelogenous leukemia; premature labor;
XX KW intrauterine infection; nutritional activity;
XX KW hematopoiesis regulating activity; tissue growth activity;
XX KW activin activity; inhibin activity; chemotactic activity;
XX KW chemokinetic activity; hemostatic activity; thrombolytic activity;
XX KW anti-inflammatory activity; splice donor site; ss.
XX
XX OS Homo sapiens.
XX
XX PN W09951744-A2.
XX
XX PD 14-OCT-1999.
XX
XX PF 05-APR-1999; 99WO-US004291.
XX
XX PR 03-APR-1998; 98US-00055010.
XX
XX PR 15-MAY-1998; 98US-00079909.
XX
XX PR 20-MAY-1998; 98US-00082364.
XX
XX PR 19-JUN-1998; 98US-00099818.
XX
XX PR 31-JUL-1998; 98US-00127698.

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PR 13-JAN-1999; 99US-00229591.
PR 17-FEB-1999; 99US-00251370.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
XX Leshkowitz D, Kita D, Ford J, Pace A, Alfénito M;
XX WPI; 1999-611042/52.
XX
XX New isolated interleukin-1 receptor binding polypeptides, used to treat
XX e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
XX inflammatory disease, autoimmune disease or proliferative disease.
XX
XX Example 8; Page 94; 123pp; English.
XX
XX AA230056-63 represent splice donor and splice acceptor sites of a genomic
XX clone encoding IL-1 receptor antagonist. The receptor antagonist
XX polynucleotides and polypeptides can be used for the prevention or
XX treatment of disorders involving sepsis, acute pancreatitis, endotoxemic
XX shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory
XX arthritis, pancreatic cell damage from diabetes mellitus type 1, graft
XX versus host disease, inflammatory bowel disease, inflammation associated
XX with pulmonary disease, other autoimmune disease or inflammatory disease,
XX an antiproliferative agent such as for acute or chronic myelogenous
XX leukemia or in the prevention of premature labor secondary to
XX intrauterine infections. They can also exhibit activities such as e.g.
XX nutritional activity, cytokine and cell proliferation/differentiation
XX activity, immune stimulating or suppressing activity, hematopoiesis
XX regulating activity, tissue growth activity, activin/inhibin activity,
XX chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
XX receptor/ligand activity, and anti-inflammatory activity. The products
XX can also be used for detection, diagnosis and drug screening
XX
XX Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
SQ

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XX Ford J, Pace A;
XX WPI; 2001-071582/08.
XX
XX Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist
XX proteins (referred as IL-1Hv1), useful in the treatment of cancer, e.g.
XX breast adenocarcinoma and brain tumors, and an inflammatory disease
XX mediated by IL-18.
XX
XX Example 8; Page 123; 179pp; English.
XX
XX The present invention relates to interleukin (IL)-1 receptor antagonist
XX proteins. IL-1Hv1 is useful for treating cancer, an inflammatory disease
XX mediated by IL-18, inflammation resulting from infection or allergic
XX reactions, and inflammation associated with chronic bronchitis,
XX arthritis, diabetes or endothermia
XX
XX Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
SQ

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XX Query Match 44.0%; Score 8.8; DB 4; Length 12;
XX Score over Length 73.3%;
XX Best Local Similarity 83.3%; Pred. No. 2.8e+06;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCCAGTTGAAG 13
DB 1 CCACAGGTGAAG 12

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XX RESULT 91
XX AAS02762
XX ID AAS02762 standard; DNA; 12 BP.
XX
XX AAS02762;
XX
XX 29-AUG-2001 (first entry)
XX
XX Human pregnane X receptor (hPXR) gene, PCR primer #32.
XX
XX Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
XX therapeutic; chemotherapy; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200120026-A2.
XX
XX 22-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-EF008827.
XX
XX 10-SEP-1999; 99EP-00118120.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Wojnowski L, Hustert E;
XX
XX WPI; 2001-273428/28.
XX
XX Novel variant of the human pregnane X receptor gene, associated with
XX insufficient metabolism and/or sensitivity to drugs, is useful for
XX diagnosing and treating diseases with drugs that are modulators of their
XX gene product.
XX
XX Claim 37; Page 39; 108pp; English.
XX
XX AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding
XX sequences and PCR primers of the invention. The human pregnane X receptor
XX sequences are used to make antibodies, or a substance capable of binding
XX specifically to the gene product of hPXR gene, for diagnosing and
XX treating various diseases, such as cancer, with drugs that are
XX substrates, inhibitors or modulators of the hPXR gene product. The
XX proteins can be used to identify and obtain prodrugs and drugs for
XX

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XX Query Match 44.0%; Score 8.8; DB 2; Length 12;
XX Score over Length 73.3%;
XX Best Local Similarity 83.3%; Pred. No. 2.8e+06;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCCAGTTGAAG 13
DB 1 CCACAGGTGAAG 12

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XX RESULT 90
XX AAF31364
XX ID AAF31364 standard; DNA; 12 BP.
XX
XX AAF31364;
XX
XX 05-APR-2001 (first entry)
XX
XX Intron/exon junction sequence #5.
XX
XX interleukin; IL-1 receptor; cancer; inflammation; ds.
XX
XX Unidentified.
XX
XX WO200102571-A2.
XX
XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018710.
XX
XX 07-JUL-1999; 99US-00348942.
XX
XX 13-OCT-1999; 99US-00417455.
XX
XX 08-DEC-1999; 99US-00457626.
XX
XX 10-MAR-2000; 2000US-00523552.
XX
XX 22-MAY-2000; 2000US-00576008.
XX
XX (HYSE-) HYSEQ INC.
XX

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CC treatment of diseases which are amenable to chemotherapy. The nucleic
CC acids can be used in gene therapy for the treatment or prevention of
CC disorders associated with hpxr expression
XX
SQ Sequence 12 BP; 2 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 4; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCCAGTTGAG 13
Db 1 CCCAGGTGAGG 12
RESULT 92
ABI22912
ID ABI22912 standard; DNA; 12 BP.
XX
AC ABI22912;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322885 for detecting SNP TSC0031095.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
DR designed to detect single-nucleotide polymorphisms and cytosine
DR methylation status.
XX
PS Claim 1; SEQ ID NO 322885; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAGTTGC 17
Db 1 AGTTGAGTTGC 17
RESULT 94
ABI23159/C
ID ABI23159 standard; DNA; 12 BP.
XX
AC ABI23159;
XX
DT 22-FEB-2002 (first entry)
XX
```

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Db 1 AGTAGAGGTGC 12
RESULT 93
ABI69899
ID ABI69899 standard; DNA; 12 BP.
XX
AC ABI69899;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 369872 for detecting SNP TSC0057857.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
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DR designed to detect single-nucleotide polymorphisms and cytosine
DR methylation status.
XX
PS Claim 1; SEQ ID NO 369872; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAGTTGC 17
Db 1 AGTTGAGTTGC 12
RESULT 94
ABI23159/C
ID ABI23159 standard; DNA; 12 BP.
XX
AC ABI23159;
XX
DT 22-FEB-2002 (first entry)
XX
```

DE Oligonucleotide primer SEQ ID NO 323132 for detecting SNP TSC0031232.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 323132; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCGCGAGTTGAA 12
Db 12 GCGCGAGTTGAA 1
RESULT 95
ABI53494
ID ABI53494 standard; DNA; 12 BP.
AC ABI53494;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 353467 for detecting SNP TSC0048527.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX

PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 353467; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 9 TCAAGTTGCCGT 20
Db 1 TGAAGTGGACGT 12
RESULT 96
ABI73838
ID ABI73838 standard; DNA; 12 BP.
XX
XX ABI73838;
AC
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 373811 for detecting SNP TSC0060333.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT

PT methylation status.
PS Claim 1; SEQ ID NO 373811; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGATTTTC 12
RESULT 97
ABH75115/C
ID ABH75115 standard; DNA; 12 BP.
XX
XX ABH75115;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 275104 for detecting SNP TSC0003785.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 275104; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGATTTTC 12
RESULT 97
ABH75115/C
ID ABH75115 standard; DNA; 12 BP.
XX
XX ABH75115;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 275104 for detecting SNP TSC0003785.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
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XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 275104; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCCCAGTTGAA 12
DB 12 GCCCCACTTTAA 1
RESULT 98
ABH90898
ID ABH90898 standard; DNA; 12 BP.
XX
XX ABH90898;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 290891 for detecting SNP TSC0014559.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 290891; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGATGTAGC 12

RESULT 99
ABI26910
ID ABI26910 standard; DNA; 12 BP.
XX
AC ABI26910;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 326883 for detecting SNP TSC0033322.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 317181; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 1 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 44.0%; Score 8.8; DB 5; Length 12;
XX Score over Length 73.3%;
XX Best Local Similarity 83.3%; Pred. No. 2.8e+06;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 1 TGAGTTGTCGT 12

RESULT 100
ABI17208/c
ID ABI17208 standard; DNA; 12 BP.
XX
AC ABI17208;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 327149 for detecting SNP TSC0033464.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 317181; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 1 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 44.0%; Score 8.8; DB 5; Length 12;
XX Score over Length 73.3%;
XX Best Local Similarity 83.3%; Pred. No. 2.8e+06;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
DB 12 TTGAGTTGCCG 1

RESULT 101
ABI27176/c
ID ABI27176 standard; DNA; 12 BP.
XX
AC ABI27176;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 327149 for detecting SNP TSC0033464.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
```

XX 06-APR-2001; 2001WO-IB000713.
XX
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
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XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
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XX Claim 1; SEQ ID NO 327149; 29pp + Sequence Listing; German.
XX
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CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 TGAAGTTGCGGT 20
DB 12 TGAAGTTGTGGT 1
RESULT 102
ABI44809
ID ABI44809 standard; DNA; 12 BP.
XX
XX ABI44809;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 344782 for detecting SNP TSC0043703.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX Oligonucleotide primer SEQ ID NO 344782 for detecting SNP TSC0043703.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
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XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 327149; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGAGATTGC 12
RESULT 103
ABI58076/c
ID ABI58076 standard; DNA; 12 BP.
XX
XX ABI58076;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 358049 for detecting SNP TSC0050929.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 358049; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGAGATTGC 12

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTCCGT 20
|||
Db 12 TGAAGTTGGAGT 1

RESULT 104

AAD52648
ID AAD52648 standard; DNA; 12 BP.

XX AAD52648;

DT 14-MAY-2003 (first entry)

XX Human ALT2 gene intron3/exon4 junction DNA.

DE Human; alanine transaminase; ALT2; diagnosis; injury; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH intron 1..6

FT /tag= a

FT /number= 3

FT /partial

FT 11..12

FT /tag= b

FT /number= 4

FT /partial

XX WO200292768-A2.

XX 21-NOV-2002.

XX 14-MAY-2002; 2002WO-US015103.

XX 14-MAY-2001; 2001US-0290829P.

XX (UYMA-) UNIV MARYLAND BALTIMORE.

XX Gong D, Shuldiner A, Yang R;

XX WPI; 2003-129280/12.

XX New human alanine transaminase polypeptide (ALT2) and gene, useful for
PT detecting injury, damage or disease involving a tissue that contains the
PT ALT2 in an animal, or in diagnosing conditions associated with altered
PT levels of ALT2.

XX Disclosure; Page 14; 57pp; English.

XX The invention relates to human alanine transaminase polypeptide (ALT2)
CC and gene. The invention is useful for diagnosing or detecting injury,
CC damage or disease involving a tissue that contains the ALT2 polypeptide
CC in an animal, in diagnosing conditions associated with altered levels of
CC ALT2 and/or ALT1 in bodily fluids. The present sequence is human ALT2
CC gene intron/exon junction DNA

XX Sequence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 8; Length 12;

Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
|||||
Db 1 CCCAGGTGATG 12

RESULT 105

AEC62435/c
ID AEC62435 standard; DNA; 12 BP.

XX AEC62435;

DT 17-NOV-2005 (first entry)

XX Human gene fragment VH1-18 mutant SEQ ID NO 45.

XX DNA sequencing; DNA amplification; DNA microarray; VH1-18; ds; mutant.

XX Homo sapiens.

XX Synthetic.

XX WO2005084134-A2.

XX 15-SEP-2005.

XX 06-MAR-2005; 2005WO-IL000263.

XX 04-MAR-2004; 2004US-0549541P.

XX (LESH/) LESHKOWITZ D.

XX Leshkowitz D;

XX WPI; 2005-639011/65.

XX Sequencing population of polynucleotide (PP) by forming hybridization
PT duplex of known oligonucleotide and PP, detecting oligonucleotide
PT involved in duplex formation and compiling set of sequences of PP.

XX Example 1; SEQ ID NO 45; 102pp; English.

XX The invention describes a method of sequencing (M1) a population of
CC polynucleotides encoding antibodies or T-cell receptors, comprising
CC contacting oligonucleotides of known sequences with population of
CC polynucleotides, to allow formation of hybridization duplexes,
CC quantitatively detecting oligonucleotides involved in formation of the
CC hybridization duplexes and compiling set of sequences of the population
CC of polynucleotides. Also described are: quantifying an expression of a
CC population of polynucleotides encoding antibodies or T-cell receptors,
CC comprising carrying out the steps of (M1), and determining a level of
CC each set of the compiled set of sequences of assembling step in the
CC population of polynucleotides, therefore quantifying the expression of
CC the population of polynucleotides encoding the antibodies or T-cell
CC receptors; and an oligonucleotide library (I) for sequencing by
CC hybridization of polynucleotides encoding variable regions of antibodies
CC or T cell receptors, comprising essentially of a set of overlapping
CC oligonucleotides collectively selected to hybridize with all germline
CC segments encoding the variable regions of the antibodies or T cell
CC receptors under conditions allowing formation of hybridization duplexes
CC between the set of overlapping oligonucleotides and the polynucleotides,
CC and variant set of oligonucleotides of the overlapping oligonucleotides,
CC which comprises (G, C, T, A) base variation in one or more positions of
CC the overlapping oligonucleotides. (M1) is useful for sequencing a
CC population of polynucleotides encoding antibodies or T-cell receptor.
CC (M1) enables a high-throughput method of sequencing a population of
CC polynucleotides that is having the ability to screen a broad spectrum of
CC samples, and allows the analysis of a large amount of cells and samples
CC in a fast manner in order to identify a number of relevant target nucleic
CC acids. This sequence represents a mutated human gene fragment VH1-18
CC associated with the sequencing method of the invention.

XX SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
||| ||| ||| |||
DB 12 CAGTTGAAGTTG 1

RESULT 106
AEC62417/c
ID AEC62417 standard; DNA; 12 BP.
XX AC AEC62417;
XX DT 17-NOV-2005 (first entry)
XX DE Human gene fragment VH1-18 mutant SEQ ID NO 27.
XX KW DNA sequencing; DNA amplification; DNA microarray; VH1-18; ds; mutant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2005084134-A2.
XX PD 15-SEP-2005.
XX PF 06-MAR-2005; 2005WO-IL000263.
XX PR 04-MAR-2004; 2004US-0549541P.
XX PA (LESH/) LESHKOWITZ D.
XX PI Leshkowitz D;
XX DR WPI; 2005-639011/65.
XX PS Sequencing population of polynucleotide (PP) by forming hybridization duplex of known oligonucleotide and PP, detecting oligonucleotide involved in duplex formation and compiling set of sequences of PP.
XX Example 1; SEQ ID NO 27; 102pp; English.
XX The invention describes a method of sequencing (M1) a population of polynucleotides encoding antibodies or T-cell receptors, comprising contacting oligonucleotides of known sequences with population of polynucleotides, to allow formation of hybridization duplexes, quantitatively detecting oligonucleotides involved in formation of the hybridization duplexes and compiling set of sequences of the population of polynucleotides. Also described are: quantifying an expression of a population of polynucleotides encoding antibodies or T-cell receptors, comprising carrying out the steps of (M1), and determining a level of each set of the compiled set of sequences of assembling step in the population of polynucleotides, therefore quantifying the expression of the population of polynucleotides encoding antibodies or T-cell receptors; and an oligonucleotide library (I) for sequencing by hybridization of polynucleotides encoding variable regions of antibodies or T cell receptors, comprising essentially of a set of overlapping oligonucleotides collectively selected to hybridize with all germline segments encoding the variable regions of the antibodies or T cell receptors under conditions allowing formation of hybridization duplexes between the set of overlapping oligonucleotides and the polynucleotides, and variant set of oligonucleotides of the overlapping oligonucleotides, which comprises (G, C, T, A) base variation in one or more positions of the overlapping oligonucleotides. (M1) is useful for sequencing a population of polynucleotides encoding antibodies or T-cell receptor. (M1) enables a high-throughput method of sequencing a population of polynucleotides that is having the ability to screen a broad spectrum of

CC samples, and allows the analysis of a large amount of cells and samples in a fast manner in order to identify a number of relevant target nucleic acids. This sequence represents a mutated human gene fragment VH1-18 associated with the sequencing method of the invention.
XX SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
||| ||| ||| |||
DB 12 CAGTTGAAGTTG 1

RESULT 107
AEC62419/c
ID AEC62419 standard; DNA; 12 BP.
XX AC AEC62419;
XX DT 17-NOV-2005 (first entry)
XX DE Human gene fragment VH1-18 mutant SEQ ID NO 29.
XX KW DNA sequencing; DNA amplification; DNA microarray; VH1-18; ds; mutant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2005084134-A2.
XX PD 15-SEP-2005.
XX PF 06-MAR-2005; 2005WO-IL000263.
XX PR 04-MAR-2004; 2004US-0549541P.
XX PA (LESH/) LESHKOWITZ D.
XX PI Leshkowitz D;
XX DR WPI; 2005-639011/65.
XX PS Sequencing population of polynucleotide (PP) by forming hybridization duplex of known oligonucleotide and PP, detecting oligonucleotide involved in duplex formation and compiling set of sequences of PP.
XX Example 1; SEQ ID NO 29; 102pp; English.
XX The invention describes a method of sequencing (M1) a population of polynucleotides encoding antibodies or T-cell receptors, comprising contacting oligonucleotides of known sequences with population of polynucleotides, to allow formation of hybridization duplexes, quantitatively detecting oligonucleotides involved in formation of the hybridization duplexes and compiling set of sequences of the population of polynucleotides. Also described are: quantifying an expression of a population of polynucleotides encoding antibodies or T-cell receptors, comprising carrying out the steps of (M1), and determining a level of each set of the compiled set of sequences of assembling step in the population of polynucleotides, therefore quantifying the expression of the population of polynucleotides encoding antibodies or T-cell receptors; and an oligonucleotide library (I) for sequencing by hybridization of polynucleotides encoding variable regions of antibodies or T cell receptors, comprising essentially of a set of overlapping oligonucleotides collectively selected to hybridize with all germline segments encoding the variable regions of the antibodies or T cell receptors under conditions allowing formation of hybridization duplexes between the set of overlapping oligonucleotides and the polynucleotides, and variant set of oligonucleotides of the overlapping oligonucleotides, which comprises (G, C, T, A) base variation in one or more positions of the overlapping oligonucleotides. (M1) is useful for sequencing a population of polynucleotides encoding antibodies or T-cell receptor. (M1) enables a high-throughput method of sequencing a population of polynucleotides that is having the ability to screen a broad spectrum of

CC the overlapping oligonucleotides. (M1) is useful for sequencing a
 CC population of polynucleotides encoding antibodies or T-cell receptor.
 CC (M1) enables a high-throughput method of sequencing a population of
 CC polynucleotides that is having the ability to screen a population of
 CC samples, and allows the analysis of a large amount of cells and samples
 CC in a fast manner in order to identify a number of relevant target nucleic
 CC acids. This sequence represents a mutated human gene fragment Vh1-18
 CC associated with the sequencing method of the invention.

XX Sequence 12 BP; 2 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 17; Length 12;
 Score over Length 73.3%;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16

Db 12 CAGCTGAAGCTG 1

RESULT 108

AEL03638

ID AEL03638 standard; DNA; 12 BP.

XX AEL03638;

XX 30-NOV-2006 (first entry)

XX Human mitochondrial DNA, D-loop, probe SEQ ID NO:357.

XX DNA detection; DNA microarray; DNA chip; SNP detection; ss;
 KW microorganism detection; cancer; cytostatic; neoplasm; infection;
 KW antimicrobial; genetic disorder; mitochondrial genome; probe.

XX Homo sapiens.

XX US7115364-B1.

XX 03-OCT-2006.

XX 02-AUG-1995; 95US-00510521.

XX 26-OCT-1993; 93US-00143312.

PR 02-AUG-1994; 94US-00284064.

PR 26-OCT-1994; 94WO-US012305.

XX (AFFY-) AFFYMETRIX INC.

XX Chee M, Cronin MT, Fodor SPA, Gingeras TR, Huang XC, Hubbell EA;
 PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;

XX WPI; 2006-706320/73.

XX Array of nucleic acid probes immobilized on solid support for comparing
 PT target nucleic acid with reference sequence, has first probe set with
 PT nucleotides complementary to reference, second probe set interrogated in
 PT first probe set.

XX Disclosure; SEQ ID NO 357; 233pp; English.

XX The invention relates to an array of nucleic acid probes immobilized on a
 CC solid support, the array comprising at least two sets or four sets of
 CC probes; a first probe set comprising several probes, each probe
 CC comprising a segment of at least six nucleotides exactly complementary to
 CC a subsequence of a reference sequence, the segment including at least one
 CC interrogation position complementary to a corresponding nucleotide in the
 CC reference sequence; a second, third and fourth probe set comprising a
 CC probe for each interrogation position in the first probe set, each probe
 CC in the second probe set being identical to a sequence comprising a
 CC corresponding probe from the first probe set or a subsequence of at least
 CC six nucleotides that includes the interrogation position, except that the
 CC interrogation position is occupied by a different nucleotide in each of

CC the two corresponding probes from the first and second probe sets. The
 CC probes in the first probe set collectively have at least three
 CC interrogation positions respectively corresponding to each of three
 CC contiguous nucleotides in the reference sequence, provided that the array
 CC does not consist of a complete set of probes of a given length. A
 CC complete set is all permutations of nucleotides A, C, G and T/U. The
 CC reference sequence is at least 50 bases, and the first probe set
 CC comprises overlapping probes spanning the reference sequence. Also
 CC included are comparing a target nucleic acid with a reference sequence
 CC comprising a predetermined sequence of nucleotides using the array of the
 CC invention, hybridizing a sample comprising the target nucleic acid to an
 CC array of nucleic acid probes immobilized on a solid support (the array
 CC comprising a set of probes comprising a first probe comprising a segment
 CC of at least 7 nucleotides exactly complementary to a subsequence of a
 CC reference sequence except at one or two positions, the segment including
 CC an interrogation position not at the one or two positions, second, third
 CC and fourth mutant probes, each identical to a sequence comprising the
 CC wild-type probe or a subsequence including the interrogation position and
 CC the one or two positions, except in the interrogation position, which is
 CC occupied by a different nucleotide in each of the four probes, provided
 CC the array does not consist of a complete set of probes of a given length,
 CC where a complete set is all permutations of nucleotides A, C, G and T/U,
 CC identifying variants of a reference sequence differing from the reference
 CC sequence in at least one nucleotide and a block of nucleic acid probes
 CC immobilized on a solid support (the array comprising a wild-type probe
 CC comprising a segment of at least six nucleotides exactly complementary to
 CC a subsequence of a reference sequence, the segment having several
 CC interrogation positions respectively corresponding to several nucleotides
 CC in the reference sequence for each interrogation position, three mutant
 CC probes, each identical to a sequence comprising the wild-type probe or a
 CC subsequence of at least six nucleotides including the several
 CC interrogation positions, except in the interrogation position, provided
 CC the array does not consist of a complete set of probes of a given length,
 CC where a complete set is all permutations of nucleotides A, C, G and T/U,
 CC where the reference sequence is from a gene having a variant form
 CC associated with development of cancer, a pathogenic microorganism, a
 CC biotransformation gene, or a gene associated with a hereditary disorder).
 CC The array of nucleic acid probes is useful for comparing target nucleic
 CC acid with a reference sequence comprising a predetermined sequence of
 CC nucleotides, where the reference sequence is a gene from an HIV virus,
 CC cystic fibrosis transmembrane indicating receptor (CFTR) gene,
 CC mitochondrial genome or biotransformation gene. The other reference
 CC sequences include p34, p65 (implicated in breast, prostate and liver
 CC cancer) and DNA segments encoding cytochromes P450 and other
 CC biotransformation genes, these reference sequences have use for forensic
 CC or epidemiological studies. Other reference sequences of interest include
 CC p34 (related to p53), p65 (implicated in breast and liver cancer), and
 CC DNA segments encoding. Other reference sequences of interest include
 CC those from the genome of pathogenic viruses (e.g., hepatitis (A, B, or
 CC C), herpes virus (e.g., VZV, HSV-1, HAV-6, HSV-II, and CMV, Epstein Barr
 CC virus), adenovirus, influenza virus, flaviviruses, echovirus, rhinovirus,
 CC genomes or episomes of pathogenic bacteria, such bacteria include
 CC Chlamydia, Rickettsia, Mycobacterium, Staphylococcus, Streptococcus,
 CC Pneumococcus, Klebsiella, Proteus, Serratia, Pseudomonas, and reference
 CC sequences in which mutations result in sickle cell anemia, beta-
 CC thalassemia, phenylketonuria, or galactosemia. The reference sequences
 CC are useful in forensic or epidemiological studies. The array is useful to
 CC read a target sequence comprising either the reference sequence itself or
 CC its variants. The present sequence is a probe for a D-loop region of the
 CC mitochondrial genome.

XX Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 19; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 2.8e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20

Db 1 TGAAGTTGCAGT 12

RESULT 109
AEL03639
ID AEL03639 standard; DNA; 12 BP.
XX AC
AC AEL03639;
XX
DT 30-NOV-2006 (first entry)
XX
XX Human mitochondrial DNA, D-loop, probe SEQ ID NO:358.
XX
XX DNA detection; DNA microarray; DNA chip; SNP detection; ss;
KW microorganism detection; cancer; cytostatic; neoplasm; infection;
KW antimicrobial; genetic disorder; mitochondrial genome; probe.
XX OS
OS Homo sapiens.
XX
XX US7115364-B1.
PN
XX
XX 03-OCT-2006.
PD
XX
XX 02-AUG-1995; 95US-00510521.
PF
XX
XX 26-OCT-1993; 93US-00143312.
PR
XX 26-OCT-1994; 94US-00284064.
PR
XX 02-AUG-1994; 94WO-US012305.
PR
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Chee M, Cronin MT, Fodor SPA, Gingeras TR, Huang XC, Hubbell EA;
PI Lipshutz RJ, Lobb PA, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
XX WPI; 2006-706320/73.
XX
XX Array of nucleic acid probes immobilized on solid support for comparing
PT target nucleic acid with reference sequence, has first probe set with
PT nucleotides complementary to reference, second probe set interrogated in
PT first probe set.
XX
XX Disclosure; SEQ ID NO 358; 233pp; English.
XX
XX The invention relates to an array of nucleic acid probes immobilized on a
CC solid support, the array comprising at least two sets or four sets of
CC probes: a first probe set comprising several probes, each probe
CC comprising a segment of at least six nucleotides exactly complementary to
CC a subsequence of a reference sequence, the segment including at least one
CC an interrogation position complementary to a corresponding nucleotide in the
CC reference sequence; a second, third and fourth probe set comprising a
CC probe for each interrogation position in the first probe set, each probe
CC in the second probe set being identical to a sequence comprising a
CC corresponding probe from the first probe set or a subsequence of at least
CC six nucleotides that includes the interrogation position, except that the
CC interrogation position is occupied by a different nucleotide in each of
CC the two corresponding probes from the first and second probe sets. The
CC probes in the first probe set collectively have at least three
CC interrogation positions respectively corresponding to each of three
CC contiguous nucleotides in the reference sequence, provided that the array
CC does not consist of a complete set of probes of a given length. A
CC complete set is all permutations of nucleotides A, C, G and T/U. The
CC reference sequence is at least 50 bases, and the first probe set
CC comprises overlapping probes spanning the reference sequence. Also
CC included are comparing a target nucleic acid with a reference sequence
CC comprising a predetermined sequence of nucleotides using the array of the
CC array of nucleic acid probes immobilized on a solid support (the array
CC comprising a set of probes comprising a first probe comprising a segment
CC of at least 7 nucleotides exactly complementary to a subsequence of a
CC reference sequence except at one or two positions, the segment including
CC an interrogation position not at the one or two positions, second, third
CC and fourth mutant probes, each identical to a sequence comprising the
CC wild-type probe or a subsequence including the interrogation position and
CC the one or two positions, except in the interrogation position, which is
CC occupied by a different nucleotide in each of the four probes, provided
CC the array does not consist of a complete set of probes of a given length,
CC

CC	where a complete set is all permutations of nucleotides A, C, G and T/U).
CC	identifying variants of a reference sequence differing from the reference
CC	sequence in at least one nucleotide and a block of nucleic acid probes
CC	immobilized on a solid support (the array comprising a wild-type probe
CC	comprising a segment of at least six nucleotides exactly complementary to
CC	a subsequence of a reference sequence, the segment having several
CC	interrogation positions respectively corresponding to several nucleotides
CC	in the reference sequence for each interrogation position, three mutant
CC	probes, each identical to a sequence comprising the wild-type probe or a
CC	subsequence of at least six nucleotides including the several
CC	interrogation positions, except in the interrogation position, provided
CC	the array does not consist of a complete set of probes of a given length,
CC	where a complete set is all permutations of nucleotides A, C, G and T/U,
CC	where the reference sequence is from a gene having a variant form
CC	associated with development of cancer, a pathogenic microorganism, a
CC	biotransformation gene, or a gene associated with a hereditary disorder).
CC	The array of nucleic acid probes is useful for comparing target nucleic
CC	acid with a reference sequence comprising a predetermined sequence of
CC	nucleotides, where the reference sequence is a gene from an HIV virus,
CC	cystic fibrosis transmembrane indicating receptor (CFTR) gene,
CC	mitochondrial genome or biotransformation gene. The other reference
CC	sequences include p34, p65 (implicated in breast, prostate and liver
CC	cancer) and DNA segments encoding cytochromes P450 and other
CC	biotransformation genes; these reference sequences have use for forensic
CC	or epidemiological studies. Other reference sequences of interest include
CC	p34 (related to p53), p65 (implicated in breast and liver cancer), and
CC	DNA segments encoding. Other reference sequences of interest include
CC	those from the genome of pathogenic viruses (e.g., hepatitis (A, B, or
CC	C), herpes virus (e.g., VZV, HSV-1, HAV-6, HSV-II, and CMV, Epstein Barr
CC	virus), adenovirus, influenza virus, flaviviruses, echovirus, rhinovirus,
CC	genomes or episomes of pathogenic bacteria, such bacteria include
CC	Chlamydia, Rickettsia, Mycobacterium, Staphylococcus, Streptococcus,
CC	Pneumococcus, Klebsiella, Proteus, Serratia, Pseudomonas, and reference
CC	sequences in which mutations result in sickle cell anemia, beta-
CC	thalassaemia, phenylketonuria, or galactosemia. The reference sequences
CC	are useful in forensic or epidemiological studies. The array is useful to
CC	read a target sequence comprising either the reference sequence itself or
CC	its variants. The present sequence is a probe for a D-loop region of the
CC	mitochondrial genome.
XX	
SQ	Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
	Query Match 44.0%; Score 8.8; DB 19; Length 12;
	Score over Length 73.3%;
	Best Local Similarity 83.3%; Pred. No. 2.8e+06;
	Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy	6 AGTTGAGATTGC 17
Db	
	1 ATTTGGAGTTGC 12
RESULT 110	
AEM30631	AEM30631 standard; RNA; 12 BP.
XX	
AC	AEM30631;
XX	
DT	08-MAR-2007 (first entry)
XX	
DE	E. coli rRNA sequence #37.
KW	RNA detection; fluorescence; protein production; bacterial infection;
KW	Escherichia coli infection; Pseudomonas aeruginosa infection; ss.
OS	Escherichia coli.
XX	
FN	WO2006122277-A2.
XX	
PD	16-NOV-2006.
XX	
PP	11-MAY-2006; 2006WO-US018320.
XX	

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PR 11-MAY-2005; 2005US-0680138P.
XX 25-AUG-2005; 2005US-0711492P.
PA (UTWA-) UNIV WAYNE STATE.
XX Cunningham PR;
XX WPI; 2007-132103/13.
XX
XX New nucleic acids that are conserved and variable regions of Escherichia
PT coli 16S rRNA, useful as targets for pharmaceuticals that are
PT taxonomically specific and/or refractory for developing drug resistance.
XX
XX Example; Fig 5.10; 232pp; English.
XX
XX The invention relates to a nucleic acid represented by a specific
CC formula. The invention also relates to a method of identifying an agent
CC that binds to a nucleic acid, a method of identifying an inhibitor of
CC protein synthesis, a compound obtained by the method and a method of
CC administering a compound to a patient in need. Identifying an agent,
CC which binds to a nucleic acid of the invention comprises measuring the
CC fluorescence of the nucleic acid, thus establishing a first fluorescence
CC reading, contacting a test compound with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a second fluorescence
CC reading, determining the difference between the first fluorescence
CC reading and the second fluorescence reading and selecting the compound
CC where the difference between the first fluorescence reading and the
CC second fluorescence reading is non-zero, thus identifying the agent. It
CC further comprises modifying the agent identified, thus forming a modified
CC agent, contacting the modified agent with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a modified second
CC fluorescence reading, determining the difference between the first
CC fluorescence reading and the modified second fluorescence reading and
CC selecting the compound where the difference between the first
CC fluorescence reading and the second modified fluorescence reading is non-
CC zero, thus identifying a modified agent. Assaying the inhibitory
CC properties of the agent comprises detecting protein synthesis or
CC determining the inhibitor constant for inhibiting mRNA translation. The
CC nucleic acids are conserved and can be used as targets for
CC pharmaceuticals that are taxonomically specific, refractory to the
CC development of drug resistance or both. They can also be used for
CC identifying an inhibitor of protein synthesis. The compound can be
CC administered to a patient having a microbial infection, preferably a
CC bacterial infection, e.g. E. coli or Pseudomonas aeruginosa infection.
XX This sequence represents E. coli rRNA used in the scope of the invention.
XX
SQ Sequence 12 BP; 3 A; 2 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 22; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 2.8e+06;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTC 16
Db 1 CAGGUGAACUUG 12

RESULT 111
AGD66526/c
ID AGD66526 standard; DNA; 12 BP.
XX
XX AGD66526;
AC
XX
XX 23-AUG-2007 (first entry)
XX Human target DNA, SEQ ID: 7.
XX
XX DNA detection; electrophoresis; ds.
XX
XX Homo sapiens.
XX
XX US2007138013-A1.
XX

PR 21-JUN-2007.
XX
XX 25-OCT-2006; 2006US-00585939.
XX
XX 26-OCT-2005; 2005JP-00311933.
XX (HAYA/) HAYASHI M.
PA (MORI/) MORI K.
PA (MAED/) MAEDA M.
XX
XX Hayashi M, Mori K, Maeda M;
XX WPI; 2007-524355/51.
XX
XX New separation device comprising electrodes, useful for DNA separation by
PT electrophoresis.
XX
XX Disclosure; SEQ ID NO 7; 21pp; English.
XX
XX The present invention provides a DNA separation device for separating
CC first sample DNA and second sample DNA by electrophoresis, the device
CC comprising a positive electrode and a negative electrode, a conjugate DNA
CC solution, and a presample solution, voltage applied to the electrodes and
CC thereby separating the DNA complexes. The invention is useful for
CC detecting a difference in portions of base sequences of DNAs and a ligand
CC DNA. The present sequence is a human target DNA from first sample DNA 5.
XX
XX Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 22; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCGATTCGAAG 13
Db 12 CCCGACCGGAAG 1

RESULT 112
AAF05404/c
ID AAF05404 standard; DNA; 17 BP.
XX
XX AAF05404;
AC
XX
XX 16-FEB-2001 (first entry)
XX
XX Hammerhead ribozyme substrate #2623.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US009721.
XX
XX 12-APR-1999; 99US-0129390P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
```

PS Claim 18; Page 116; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TP2 Orphan receptor, EAR3/COUP-TP-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha

XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 3; Length 17;

Score over Length 72.9%;

Best Local Similarity 92.9%; Pred. No. 5e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17

DB 15 CCAGTTGAAGCTGC 2

RESULT 113

AAFP05403/C
ID AAF05403 standard; DNA; 17 BP.

XX AAF05403;

XX 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #2622.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.

XX Homo sapiens.

PN WO200061729-A2.

PD 19-OCT-2000.

XX 11-APR-2000; 2000WO-US0009721.

PR 12-APR-1999; 99US-0129390P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Zwick M, Pavco P, Mcswiggen J;

XX WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.

PS Claim 18; Page 116; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TP2 Orphan receptor, EAR3/COUP-TP-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha

XX Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 3; Length 17;

Score over Length 72.9%;

Best Local Similarity 92.9%; Pred. No. 5e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17

DB 16 CCAGTTGAAGCTGC 3

RESULT 114

AEH24548/c

ID AEH24548 standard; DNA; 22 BP.

XX AEH24548;

XX 29-JUN-2006 (first entry)

DE BAX gene forward PCR primer.

XX ss; PCR; primer; drug metabolism; cancer; cytostatic; neoplasm;
KW immune inhibition; apoptosis stimulation; RNA quantitation; BAX.

XX Homo sapiens.

PN WO2006045053-A2.

XX 27-APR-2006.

XX 20-OCT-2005; 2005WO-US037925.

XX 20-OCT-2004; 2004US-0620603P.

PR 16-FEB-2005; 2005US-0653557P.

PR 08-JUN-2005; 2005US-0688741P.

XX (HITB) HITACHI CHEM CO LTD.

XX (HITB) HITACHI CHEM RES CENT INC.

XX Mitsuhashi M;

XX WPI; 2006-332057/34.

XX Measuring a patient's responsiveness to a drug comprises exposing whole
PT blood of the patient to the drug for 7 hours or less, and measuring the
PT amount of an mRNA associated with an effect of the drug in blood cells.

XX Disclosure; SEQ ID NO 39; 74pp; English.

XX The invention relates to a method of measuring a patient's responsiveness
CC to a which drug comprises exposing whole blood of the patient to the drug
CC for 7 hours or less, and measuring the amount of an mRNA associated with
CC an effect of the drug in blood cells. Preferably, the amount of the mRNA
CC present in the blood cells is measured before the exposure, and the
CC change in the amount of the mRNA is determined by comparing the amount of
CC mRNA measured before exposure to the amount of mRNA measured after
CC exposure. The method additionally comprises exposing whole blood of the
CC patient to a control vehicle for 7 hours or less; after the exposure,
CC measuring the amount of the mRNA associated with an effect of the drug in
CC the blood cells exposed to the control vehicle; and identifying
CC responsiveness to the drug includes comparing results of the measurement
CC obtained after exposure to the control vehicle with results of the
CC measurement obtained after exposure to the drug. The control vehicle is
CC selected from phosphate-buffered saline and dimethyl sulfoxide. The mRNA
CC is selected from mRNAs encoding the gene products of the Bcl-2/Bax gene
CC family, Bax gene product, the Bcl-2 gene family, ATP-binding
CC cassette subfamilies A to G, and p21, PUMA and NOXA gene products. The
CC method is useful for measuring a patient's responsiveness to a drug,
CC which is useful in developing an optimized treatment protocol tailored to
CC the specific patient. The method may be used for patients with conditions
CC such as cancer or diseases which require immunosuppression. The present
CC sequence represents BAX gene forward PCR primer. This gene was amplified
CC in studies of drug induced apoptosis in tailored drug administration for
CC leukemia and lymphoma.

XX Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 22;

Score over Length 72.7%; Pred. No. 8.9e+02; DB 19; Length 22;
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 115
AEH24560/c
ID AEH24560 standard; DNA; 22 BP.
AC AEH24560;
XX
DT 29-JUN-2006 (first entry)
XX
DE BAX forward real-time PCR primer.
XX
KW ss; PCR; primer; drug metabolism; cancer; cytostatic; neoplasm;
KW immune inhibition; apoptosis stimulation; RNA quantitation; BAX.
XX
OS Homo sapiens.
XX
PN WO2006045053-A2.
XX
PD 27-APR-2006.
XX
PP 20-OCT-2005; 2005WO-US037925.
XX
PR 20-OCT-2004; 2004US-0620603P.
PR 16-FEB-2005; 2005US-0653557P.
PR 08-JUN-2005; 2005US-0688741P.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (HITB) HITACHI CHEM RES CENT INC.
XX
PI Mitsubishi M;
XX
DR WPI; 2006-332057/34.
XX
PT Measuring a patient's responsiveness to a drug comprises exposing whole
PT blood of the patient to the drug for 7 hours or less, and measuring the
PT amount of an mRNA associated with an effect of the drug in blood cells.
XX
PS Disclosure; SEQ ID NO 51; 74pp; English.
XX
CC The invention relates to a method of measuring a patient's responsiveness
CC to a which drug comprises exposing whole blood of the patient to the drug
CC for 7 hours or less, and measuring the amount of an mRNA associated with
CC an effect of the drug in blood cells. Preferably, the amount of the mRNA
CC present in the blood cells is measured before the exposure, and the
CC change in the amount of the mRNA is determined by comparing the amount of
CC mRNA measured before exposure to the amount of mRNA measured after
CC exposure. The method additionally comprises exposing whole blood of the
CC patient to a control vehicle for 7 hours or less; after the exposure,
CC measuring the amount of the mRNA associated with an effect of the drug in
CC the blood cells exposed to the control vehicle; and identifying
CC responsiveness to the drug includes comparing results of the measurement
CC obtained after exposure to the control vehicle with results of the
CC measurement obtained after exposure to the drug. The control vehicle is
CC selected from phosphate-buffered saline and dimethyl sulfoxide. The mRNA
CC is selected from mRNAs encoding the gene products of the Bcl-2/Bax gene
CC family, Bax gene product, the BH3-only Bcl-2 gene family, ATP-binding
CC cassette subfamilies A to G, and p21, PUMA and NOXA gene products. The
CC method is useful for measuring a patient's responsiveness to a drug,
CC which is useful in developing an optimized treatment protocol tailored to
CC the specific patient. The method may be used for patients with conditions
CC such as cancer or diseases which require immunosuppression. The present
CC sequence represents BAX forward real-time PCR primer, used in RNA
CC quantitation of BAX in assessment of leukocyte suppression.
XX
SQ Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 22;
Score over Length 72.7%;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 116
AEJ10474/c
ID AEJ10474 standard; DNA; 22 BP.
XX
AC AEJ10474;
XX
DT 07-SEP-2006 (first entry)
XX
DE Antisense PCR primer for RCR from 3-way junction structure.
XX
KW DNA detection; microorganism detection; SNP detection;
KW epigenetic modification; diagnostic; RNA detection; DNA amplification;
KW DNA methylation; gene amplification; primer extension; primer; PCR;
KW antisense; ss.
XX
OS Synthetic.
XX
PN WO2006074162-A2.
XX
PD 13-JUL-2006.
XX
PP 04-JAN-2006; 2006WO-US000086.
XX
PR 04-JAN-2005; 2005US-0641255P.
PR 14-JUL-2005; 2005US-0699340P.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (HITB) HITACHI CHEM RES CENT INC.
XX
PI Murakami T;
XX
DR WPI; 2006-513365/52.
XX
PT Amplifying nucleic acid, by combining a nucleic acid primer with a
PT polymerase and a circular nucleic acid probe, and producing a repeat of a
PT sequence copy of the circular nucleic acid probe.
XX
PS Example 2; SEQ ID NO 6; 34pp; English.
XX
CC The present invention discloses a method of amplifying nucleic acid using
CC primers and probes by rolling circle amplification method. The present
CC invention comprises primer generation ? rolling circle amplification (PG-
CC RCA) in which a ribbon probe is involved, allows the single step
CC detection of nucleic acid sequences such as DNA and RNA sensitively and
CC rapidly. This technology is easily applicable to detection of other
CC biomolecules such as DNA methylation, single nucleotide polymorphism
CC (SNP), protein and posttranslational modifications. PCR (primer
CC generation) reaction is a reaction that is designed to produce at least
CC one nucleic acid primer from a PGR initiation sequence of an RCR (rolling
CC circle reaction) product and the resulting primer is designed to prime to
CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is
CC designed to produce concatenated sequence copies of the circular probe,
CC in which the resulting product contains at least one PGR initiation
CC sequence in every repeat sequence just like the initial reaction signal.
CC The first and second nucleic acid primers are generated by one of
CC nuclease-based cleavage reaction, strand displacement amplification,
CC cleavage-initiated isothermal amplification, three-way junction
CC isothermal amplification, three-way junction rolling circle reaction,
CC binding assay using a nucleic acid labeled recognition agent and
CC proximity assay. The method of nucleic acid detection using the present
CC invention is useful for in vitro diagnostics and in pathogen detection.
CC The nucleotide sequence presented here is the antisense PCR primer for

```
CC RCR from 3-way junction structure.
XX
SQ Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match      80.0%; Score 16; DB 19; Length 22;
  Score over Length 72.7%;
  Best Local Similarity 100.0%; Pred. No. 8.9e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 117
ABC96949/c
ID ABC96949 standard; DNA; 13 BP.
XX
AC ABC96949;
XX
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 96966 for detecting SNP TSC0024054.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 96966; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 13;
  Score over Length 72.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
Db 13 TGAAGTTGCCG 3

RESULT 118
ABC25038
ID ABC25038 standard; DNA; 13 BP.
XX
XX ABC25038;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 25055 for detecting SNP TSC0006071.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 25055; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 13;
  Score over Length 72.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
Db 3 TGAAGTTGCCG 13

RESULT 119
ABF17290
ID ABF17290 standard; DNA; 13 BP.
XX
XX ABF17290;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 117287 for detecting SNP TSC0029345.
XX
```

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 117287; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
DB 3 AGTTGAGTTG 13
RESULT 120
ABF17291/C
ID ABF17291 standard; DNA; 13 BP.
XX
XX ABF17291;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 117288 for detecting SNP TSC0029345.
DE
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX

PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 117288; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
DB 11 AGTTGAGTTG 1
RESULT 121
ABF17512
ID ABF17512 standard; DNA; 13 BP.
XX
XX ABF17512;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 117509 for detecting SNP TSC0029385.
DE
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

PS Claim 1; SEQ ID NO 117509; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||

Db 3 AGTTGAAGTTG 13
|||||

RESULT 122

ABC27952

ID ABC27952 standard; DNA; 13 BP.

XX

AC ABC27952;

XX

DT 20-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 27969 for detecting SNP TSC0007879.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPTG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX

Claim 1; SEQ ID NO 27969; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||

Db 3 AGTTGAAGTTG 13
|||||

RESULT 123

ABH35811/C

ID ABH35811 standard; DNA; 13 BP.

XX

AC ABH35811;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 235788 for detecting SNP TSC0009202.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX

Claim 1; SEQ ID NO 235788; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||

```
Db      13 AGTGAAGTTG 3
RESULT 124
ABF11324
ID      ABF11324 standard; DNA; 13 BP.
XX
AC      ABF11324;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 111321 for detecting SNP TSC0027809.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 111321; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy      6 AGTGAAGTTG 16
Db      3 AGTTGAGTTG 13
RESULT 125
ABH15808
ID      ABH15808 standard; DNA; 13 BP.
XX
AC      ABH15808;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 215785 for detecting SNP TSC0052481.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 111321; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy      6 AGTGAAGTTG 16
Db      3 AGTTGAGTTG 13
```

```
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 215785; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy      6 AGTGAAGTTG 16
Db      1 AGTTGAGTTG 11
RESULT 126
ABH48372
ID      ABH48372 standard; DNA; 13 BP.
XX
AC      ABH48372;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 248349 for detecting SNP TSC0060684.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
```

```

XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 248349; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX Score over Length 72.3%;
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTTG 16
XX DB 1 AGTTGAGTTG 11
XX RESULT 127
XX ABC25065/C
XX ID ABC25065 standard; DNA; 13 BP.
XX AC ABC25065;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 25082 for detecting SNP TSC0006096.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 248349; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX Score over Length 72.3%;
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTTG 16
XX DB 1 AGTTGAGTTG 11
XX RESULT 128
XX ABC06232
XX ID ABC06232 standard; DNA; 13 BP.
XX AC ABC06232;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 6223 for detecting SNP TSC0001948.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 6223; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX Score over Length 72.3%;
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTTG 16
XX DB 12 AGTGAAGTTG 2

```

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTTG 16
|||||
Db 3 AGTAGAAGTTG 13
|||||

RESULT 129
ABC25039/C
ID ABC25039 standard; DNA; 13 BP.

XX AC ABC25039;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 25056 for detecting SNP TSC0006071.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 25056; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 TGAAGTTGCG 19

Db 11 TGAAGTTGCG 1
|||||

RESULT 130
ABC56736

ID ABC56736 standard; DNA; 13 BP.

XX AC ABC56736;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 56753 for detecting SNP TSC0015377.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 56753; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTTG 16
|||||

Db 1 AGTTGAAGTTG 11
|||||

RESULT 131
ABC96948

ID ABC96948 standard; DNA; 13 BP.

XX AC ABC96948;

XX DT 21-FEB-2002 (first entry)

XX

PT methylation status.
XX
PS Claim 1; SEQ ID NO 36538; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
Dd | ||||| |||||
13 ATTGAAGTTG 3
RESULT 134
ABH48373/C
ID ABH48373 standard; DNA; 13 BP.
XX
AC ABH48373;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 248350 for detecting SNP TSC0060684.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX Oligonucleotide SEQ ID NO 248350 for detecting SNP TSC0060684.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.
XX
XX Claim 1; SEQ ID NO 248350; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
Dd | ||||| |||||
13 ATTGAAGTTG 3
RESULT 135
ABC36520
ID ABC36520 standard; DNA; 13 BP.
XX
AC ABC36520;
XX
XX 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 36537 for detecting SNP TSC0011456.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.
XX
XX Claim 1; SEQ ID NO 36537; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 215786; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX PS Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX XX
XX CC Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX CC Score over Length 72.3%;
XX CC Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTTG 16
XX DB ||||| |||||
XX 13 AGTTGAGTTG 3
XX
XX RESULT 139
XX ABC25064
XX ID ABC25064 standard; DNA; 13 BP.
XX AC ABC25064;
XX XX
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 25081 for detecting SNP TSC0006096.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 25081 for detecting SNP TSC0006096.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPiG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 215786; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX PS Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX XX
XX CC Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX CC Score over Length 72.3%;
XX CC Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTTG 16
XX DB ||||| |||||
XX 13 AGTTGAGTTG 3
XX
XX RESULT 140
XX ABF17513/C
XX ID ABF17513 standard; DNA; 13 BP.
XX XX
XX AC ABF17513;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 117510 for detecting SNP TSC0029385.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPiG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 117510; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX PS Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX XX
XX CC Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX CC Score over Length 72.3%;
XX CC Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTTG 16
XX DB ||||| |||||
XX 2 AGTTGAAGTTG 12
XX
XX RESULT 140
XX ABF17513/C
XX ID ABF17513 standard; DNA; 13 BP.
XX XX
XX AC ABF17513;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 117510 for detecting SNP TSC0029385.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPiG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 117510; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
```

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 11 AGTTGAAGTTG 1

RESULT 141
ABH35810
ID ABH35810 standard; DNA; 13 BP.

XX AC ABH35810;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 235787 for detecting SNP TSC0009202.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 235787; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 1 AGTTGAAGTTG 11

RESULT 142
ABC12623/C

XX ID ABC12623 standard; DNA; 13 BP.

XX AC ABC12623;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 12630 for detecting SNP TSC0002968.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 12630; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 12 AGTTGAAGTTG 2

RESULT 143
ABF11325/C

XX ID ABF11325 standard; DNA; 13 BP.

XX AC ABF11325;

XX XX

DT 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 111322 for detecting SNP TSC0027809.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 111322; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTTG 16
Db 11 AGTTGACTTG 1
RESULT 144
ABC27953/c
ID ABC27953 standard; DNA; 13 BP.
XX
XX ABC27953;
AC
XX
XX 20-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 27970 for detecting SNP TSC0007879.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
XX

PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 27970; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTTG 16
Db 13 AGTTGAATG 3
RESULT 145
ABC06233/c
ID ABC06233 standard; DNA; 13 BP.
XX
XX ABC06233;
AC
XX
XX 20-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 6224 for detecting SNP TSC0001948.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX

CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance/quality control of
 CC bacterial contamination, monitoring microbiological assays, tracing bacterial
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI
 CC restriction site and used in the method of the invention.

XX SQ Sequence 13 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 1 Other;
 Query Match 47.0%; Score 9.4; DB 13; Length 13;
 Score over Length 72.3%;
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
 ||||| |||||
 Db 13 CCCAGTSGAAG 3

RESULT 148
 ADR35834/c
 ID ADR35834 standard; DNA; 13 BP.
 XX AC ADR35834;
 XX DT 04-NOV-2004 (first entry)
 XX DE Human nicking agent DNA containing BstNBI restriction site #2254.

XX ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.

XX OS Homo sapiens.
 XX FN WO2004067765-A2.
 XX PD 12-AUG-2004.

XX PF 29-JAN-2004; 2004WO-US002720.
 XX PR 29-JAN-2003; 2003US-0443811P.
 XX PA (KECK-) KECK GRADUATE INST.

XX PI Van Ness J, Galas DJ, Van Ness LK;
 XX DR WPI; 2004-581010/56.

XX PT Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.

XX PS Example 3; Page 105-219; 238pp; English.

XX CC The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly

CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance/quality control of
 CC bacterial contamination, monitoring microbiological assays, tracing bacterial
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI
 CC restriction site and used in the method of the invention.

XX SQ Sequence 13 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 1 Other;
 Query Match 47.0%; Score 9.4; DB 13; Length 13;
 Score over Length 72.3%;
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
 ||||| |||||
 Db 13 CCCAGTSGAAG 3

RESULT 149
 ADR35835/c
 ID ADR35835 standard; DNA; 13 BP.

XX AC ADR35835;
 XX DT 04-NOV-2004 (first entry)
 XX DE Human nicking agent DNA containing BstNBI restriction site #2255.

XX ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.

XX OS Homo sapiens.
 XX FN WO2004067765-A2.
 XX PD 12-AUG-2004.

XX PF 29-JAN-2004; 2004WO-US002720.
 XX PR 29-JAN-2003; 2003US-0443811P.
 XX PA (KECK-) KECK GRADUATE INST.

XX PI Van Ness J, Galas DJ, Van Ness LK;
 XX DR WPI; 2004-581010/56.

XX PT Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.

XX PS Example 3; Page 105-219; 238pp; English.

XX CC The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA

molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 The method, kit or composition is useful for identifying the source
 organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 non-human animal or human. The method is particularly useful for rapidly
 fingerprinting DNA to identifying prokaryotic and eukaryotic species.
 subpecies, and especially strains or individuals of the subpecies. It
 is especially useful for identifying different bacterial strains involved
 in e.g., nosocomial infections. Furthermore, the method is useful for
 diagnosing bacterial disease in plants and humans, monitoring for
 bacterial contamination, monitoring quality assurance/quality control of
 laboratory tests involving microbiological assays, tracing bacterial
 contamination and/or outbreaks of bacterial infections, genome mapping,
 monitoring bioremediation sites, and for monitoring agricultural sites
 for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 ADR37496 correspond to target nucleic acids containing an NBstNBI
 restriction site and used in the method of the invention.

Query Match 47.0%; Score 9.4; DB 13; Length 13;
 Score over Length 72.3%;
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
 ||||| ||||
 Db 13 CCCAGTSGAAG 3

RESULT 150
 ADR35832/c
 ID ADR35832 standard; DNA; 13 BP.
 XX
 AC ADR35832;
 DT 04-NOV-2004 (first entry)
 DE Human nicking agent DNA containing BstNBI restriction site #2252.
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 PN WO2004067765-A2.
 PD 12-AUG-2004.
 XX 29-JAN-2004; 2004WO-US0002720.
 PF 29-JAN-2003; 2003US-0443811P.
 PR (KECK-) KECK GRADUATE INST.
 PA Van Ness J, Galas DJ, Van Ness LX;
 PI WPI; 2004-581010/56.
 DR Identifying nucleic acid sample source, useful for identifying bacterial
 XX strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX Example 3; Page 105-219; 238pp; English.
 PS The invention relates to a method of treating a nucleic acid sample with
 XX components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the

family of initiating oligonucleotide fragments to a characterization
 process to thus provide results. The method is useful for creating an
 assay panel of diagnostic oligonucleotides that can identify any organism
 or individual. The method is useful for characterizing other DNA
 molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 The method, kit or composition is useful for identifying the source
 organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 non-human animal or human. The method is particularly useful for rapidly
 fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 subpecies, and especially strains or individuals of the subpecies. It
 is especially useful for identifying different bacterial strains involved
 in e.g., nosocomial infections. Furthermore, the method is useful for
 diagnosing bacterial disease in plants and humans, monitoring for
 bacterial contamination, monitoring quality assurance/quality control of
 food for bacterial contamination, monitoring quality assurance/quality control of
 bacterial contamination, monitoring microbiological assays, tracing bacterial
 laboratory tests involving microbiological assays, genome mapping,
 contamination and/or outbreaks of bacterial infections, tracing bacterial
 monitoring bioremediation sites, and for monitoring agricultural sites
 for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 ADR37496 correspond to target nucleic acids containing an NBstNBI
 restriction site and used in the method of the invention.

Query Match 47.0%; Score 9.4; DB 13; Length 13;
 Score over Length 72.3%;
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
 ||||| ||||
 Db 13 CCCAGTSGAAG 3

RESULT 151
 ADQ80013/c
 ID ADQ80013 standard; DNA; 17 BP.
 XX
 AC ADQ80013;
 XX 09-SEP-2004 (first entry)
 DT A. Kurodai octopamine receptor associated primer #8.
 DE ss; PCR; primer; octopamine receptor; PKA pathway;
 KW CAMP-dependent protein kinase; short-term memory.
 XX Synthetic.
 OS KR2004019613-A.
 PN 06-MAR-2004.
 PD 28-AUG-2002; 2002KR-00051211.
 PF 28-AUG-2002; 2002KR-00051211.
 PR (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX Jang DJ, Kang BG;
 PI WPI; 2004-45652/44.
 XX Octopamine receptor isolated from aplysia kurodai and activation method
 PT of pka (camp-dependent protein kinase) pathway.
 PT Disclosure; SEQ ID NO 8; 32pp; Korean.
 PS The invention relates to an octopamine receptor isolated from Aplysia
 XX kurodai and an activation method of PKA (CAMP-dependent protein kinase)
 CC pathway. The method improves short-term memory and screens a drug
 CC activating the PKA pathway to improve memory. The present sequence

CC represents an A. kurodai octopamine receptor associated primer.

SQ Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 13; Length 17;

Score over Length 71.8%;

Best Local Similarity 82.4%; Pred. No. 6.3e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCCGAGTTGAGTTGCC 18

DB 17 CACGAGTTGAGTAGCC 1

RESULT 152

AAQ83300
ID AAQ83300 standard; DNA; 14 BP.

XX AC

XX AAQ83300;

XX DT 25-MAR-2003 (revised).

XX DT 20-SEP-1995 (first entry)

XX DE c-jun antisense oligonucleotide.

XX KW c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;

XX KW phosphorothioate; ss.

XX OS Synthetic.

XX PN WO9502051-A2.

XX XX 19-JAN-1995.

XX PF 06-JUL-1994; 94WO-EP002218.

XX PR 10-JUL-1993; 93EP-00111059.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;

XX DR WPI; 1995-066896/09.

XX Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and treating neuronal injury, degeneration, cell death and/or neoplasms.

XX PS Claim 2; Page 30; 86pp; English.

CC Antisense nucleic acid hybridising with an area of the mRNA and/or DNA comprising the genes c-jun, jun-B or c-fos, expression of which plays a causal role in neuronal injury, degeneration, cell death and/or neoplasms, can be used to prevent and treat such conditions. c-jun antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B antisense sequences are described in AAQ83322-363 and AAQ83444-45; and c-fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51. Preferably the antisense sequences are phosphorothioate oligonucleotides since these are not destroyed as fast by endogenous factors as naturally occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 14 BP; 2 A; 1 C; 6 G; 5 T; 0 U; 0 Other;

Query Match

Score over Length 50.0%; Score 10; DB 2; Length 14;

Best Local Similarity 71.4%;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

DB 5 GTTGAAGTTG 14

RESULT 153

Query Match

Score over Length 85.0%; Score 17; DB 19; Length 24;

Best Local Similarity 70.8%;

Pred. No. 2.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20
|||||
Db 1 CCAGTTGAAGTTGCCGT 17

RESULT 154
AEJ10484
ID AEJ10484 standard; DNA; 24 BP.
XX
AC AEJ10484;
XX
DT 07-SEP-2006 (first entry)
XX
DE Target nucleic acid used in PG-RCA using ribbon probe.
XX
KW DNA detection; microorganism detection; SNP detection;
KW epigenetic modification; diagnostic; RNA detection; DNA amplification;
KW DNA methylation; gene amplification; primer extension; ss;
KW DNA-RNA hybrid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 22..24
FT /*tag= a
FT modified_base 22..24
FT /*tag= b
FT /*mod_base= 2'-O-methyluridine
XX
PN WO2006074162-A2.
XX
PD 13-JUL-2006.
XX
PF 04-JAN-2006; 2006WO-US000086.
XX
PR 04-JAN-2005; 2005US-0641255P.
PR 14-JUL-2005; 2005US-0699340P.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (HITB) HITACHI CHEM RES CENT INC.
XX
PI Murakami T;
XX
WPI; 2006-513365/52.
XX
Amplifying nucleic acid, by combining a nucleic acid primer with a
polymerase and a circular nucleic acid probe, and producing a repeat of a
sequence copy of the circular nucleic acid probe.

Example 6; SEQ ID NO 16; 34pp; English.

The present invention discloses a method of amplifying nucleic acid using
primers and probes by rolling circle amplification method. The present
invention comprises primer generation, rolling circle amplification (PG-
RCA) in which a ribbon probe is involved, allows the single step
detection of nucleic acid sequences such as DNA and RNA sensitively and
rapidly. This technology is easily applicable to detection of other
biomolecules such as DNA methylation, single nucleotide polymorphism
(SNP), protein and posttranslational modifications. PCR (primer
generation reaction) is a reaction that is designed to produce at least
one nucleic acid primer from a PCR initiation sequence of an RCR (rolling
circle reaction) product and the resulting primer is designed to prime to
a circular nucleic acid probe and initiate RCR. On the other hand, RCR is
designed to produce concatenated sequence copies of the circular probe,
in which the resulting product contains at least one PCR initiation
sequence in every repeat sequence just like the initial reaction signal.
The first and second nucleic acid primers are generated by one of
nuclease-based cleavage reaction, strand displacement amplification,
cleavage-initiated isothermal amplification, three-way junction
isothermal amplification, three-way junction rolling circle reaction,
binding assay using a nucleic acid labeled recognition agent and

CC proximity assay. The method of nucleic acid detection using the present
invention is useful for in vitro diagnostics and in pathogen detection.
CC The nucleotide sequence presented here is the target nucleic acid used in
CC PG-RCA using ribbon probe.
XX
SQ Sequence 24 BP; 5 A; 5 C; 6 G; 5 T; 3 U; 0 Other;
Query Match 85.0%; Score 17; DB 19; Length 24;
Score over Length 70.8%;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20
|||||
Db 1 CCAGTTGAAGTTGCCGT 17

RESULT 155
ABS64186
ID ABS64186 standard; DNA; 15 BP.
XX
AC ABS64186;
XX
DT 15-NOV-2002 (first entry)
XX
DE Tachykinin receptor gene TACR2, allele-specific probe #24.
DE XX
KW Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;
KW tachykinin receptor.
XX
OS Homo sapiens.
XX
PN WO200263046-A1.
XX
PD 15-AUG-2002.
XX
PF 09-NOV-2001; 2001WO-US047394.
XX
PR 09-NOV-2000; 2000US-0247649P.
XX
PA (GENA-) GENAISANCE PHARM INC.
XX
PI Cappola G, Chew A, Gilson CR, Koshy B;
XX
WPI; 2002-636600/68.
XX
New genetic variants having polymorphisms in the Tachykinin receptor
(TACR2) protein, useful for studying the function of TACR2, and for
treating disorders associated with abnormal expression or function of
TACR2 isogene.

Claim 14; Page 14; 130pp; English.

The invention relates to an isolated polypeptide comprising a polymeric
variant of a reference sequence for the Tachykinin receptor (TACR2)
protein. Also described is a method for: (1) haplotyping or genotyping
the TACR2 gene of an individual; (2) predicting a haplotype pair for the
TACR2 gene of an individual; (3) identifying an association between a
trait and at least one haplotype or haplotype pair of the TACR2 gene; and
(4) isolated oligonucleotide for detecting a single nucleotide
polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene
are useful in studying the expression and biological function of TACR2,
and in identifying drugs targeting TACR2 protein for treating disorders
associated with abnormal expression or function of TACR2, e.g. asthma or
breast cancer. Polynucleotides comprising a polymorphic gene variant or
fragment may be used for therapeutic purposes, where a patient could
benefit from expression or increased expression of a particular TACR2
protein isoform, or an expression vector encoding the isoform may be
administered to the patient. Haplotype information is useful in improving
the efficiency and output of several steps in drug discovery and
development process, including target validation, identifying lead
compounds, and early phase clinical trials. Information on polymorphisms
may be applied in studying biological functions of TACR2 as well as in

CC identifying drugs targeting this protein for the treatment of disorders
CC related to its abnormal expression or function. ABS64163-ABS64302
CC represent human TACR2 gene allele-specific oligonucleotide probes and
CC primers used to detect haplotypes of the TACR2 gene of the invention
XX
SQ Sequence 15 BP; 3 A; 3 C; 4 G; 4 T; 0 U; 1 Other;

Query Match 53.0%; Score 10.6; DB 6; Length 15;
Score over Length 70.7%;
Best Local Similarity 90.9%; Pred. No. 3.8e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
||||:|||||
DB 4 CCA GTTGAAGT 14

RESULT 156
AAX71130/c
ID AAX71130 standard; RNA; 17 BP.
XX AC
AC AAX71130;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #142.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 101; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 5 A; 3 C; 4 G; 4 T; 5 U; 0 Other;

Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAGT 14
||||:|||||
DB 17 CCAGTTGAAGT 6

RESULT 158
AEB61076/c
ID AEB61076 standard; mRNA; 17 BP.

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAGT 14
||||:|||||
DB 16 CCAGTTGAAGT 5

RESULT 157
AAX71129/c
ID AAX71129 standard; RNA; 17 BP.
XX AC
AC AAX71129;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #141.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 101; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAGT 14
||||:|||||
DB 17 CCAGTTGAAGT 6

RESULT 158
AEB61076/c
ID AEB61076 standard; mRNA; 17 BP.

XX AC AEB61076;
XX DT 22-SEP-2005 (first entry)
XX DE Human VEGF receptor 21 (Kdr) DNazyme target sequence SEQ ID 3654.
XX KW VEGF receptor; angiogenesis; cancer; tumor; ocular disease;
KW diabetic retinopathy; age related macular degeneration;
KW angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing;
KW endometriosis; endometrial carcinoma; gynecological bleeding disorder;
KW menorrhagia disorder; premenstrual syndrome; menopause; gynecological;
KW Cystostatic; Ophthalmological; Antidiabetic; antitumor; Antipsoriatic; Antirheumatic; Antiarthritic; Vulnerary; Hemostatic;
KW Contraceptive; ss; enzymatic nucleic acid.
XX OS Homo sapiens.
XX SS WO200296927-A2.
XX PN 05-DEC-2002.
XX PD 29-MAY-2002; 2002WO-US017674.
XX PF 29-MAY-2001; 2001US-00870161.
XX PR 30-NOV-2001; 2001US-0334461P.
XX PR 03-MAY-2002; 2002US-00138674.
XX XX (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR) CHIRON CORP.
XX PI Escobedo J, Mcswiggen J, Pavco P, Stinchcomb D, Sandberg J;
PI Gordon G;
XX WPI; 2003-140439/13.
XX DR Novel enzymatic nucleic acids, ribozymes, which modulate expression of
XX PT genes encoding vascular endothelial growth factor and/or VEGF receptor,
XX PT useful for inhibiting tumor angiogenesis in cell, and for treating
XX PT cancer.
XX PS Disclosure; SEQ ID NO 3654; 172pp; English.
XX CC The invention relates to enzymatic nucleic acids (I) i.e.
XX CC ribozymes/DNAzymes/Zinczymes that target and modulate expression of, genes
XX CC encoding vascular endothelial growth factor (VEGF) and/or VEGF receptor
XX CC (VEGFRI and 2 encode by the Flt-1 and Kdr genes respectively). Also
XX CC included are a composition comprising (I) and a carrier, administering
XX CC (I) to a cell (by contacting the cell with the compound under conditions
XX CC suitable for the administration), administering (I) to a cell (in
XX CC conjunction with one or more other drug by contacting the cell with the
XX CC compound and the other drug under conditions suitable for the
XX CC administration), administering (I) to a mammal (by contacting the mammal
XX CC with the compound under conditions suitable for the administration),
XX CC treating (M1) a subject having endometriosis (by contacting a subject
XX CC with, or administering to subject, a nucleic acid molecule (II) that
XX CC modulates expression of VEGF, VEGFR1, and/or VEGFR2), a mammalian cell
XX CC (III) comprising (I) and administering to a mammal (I) (in conjunction
XX CC with a chemotherapeutic agent comprising contacting the mammal with the
XX CC compound and the chemotherapeutic agent under conditions suitable for the
XX CC administration), (I) is administered to a mammalian cell, preferably
XX CC human cell in the presence of a delivery reagent which is a lipid such as
XX CC cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acid
XX CC molecule has an endonuclease activity to cleave RNA encoded by an VEGFR1
XX CC or VEGFR2 gene, and is in a hammerhead, inozyme, DNazyme, G-cleaver,
XX CC or Ambezyme configuration. The enzymatic nucleic acids are useful for
XX CC inhibiting ocular angiogenesis associated with diabetic retinopathy or
XX CC age-related diabetic retinopathy, in a subject. They are also useful for
XX CC inhibiting angiogenesis, preferably tumor angiogenesis in cell, and for
XX CC treating a subject having a condition associated with an increased level
XX CC of VEGF receptor, where the condition is cancer, e.g. breast cancer, lung
XX CC cancer (such as non-small cell lung carcinoma), colorectal cancer, renal
XX CC cancer (such as renal cell carcinoma), pancreatic cancer. The enzymatic

CC nucleic acids are useful for treating a subject (preferably human) having
CC endometriosis, psoriasis, age-related macular degeneration, proliferative
CC diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis,
CC wound healing, endometrial carcinoma, gynecologic bleeding disorders,
CC irregular menstrual cycles, ovulation, premenstrual syndrome, and
CC menopaual dysfunction. The enzymatic nucleic acids are useful for birth
CC control by inhibiting ovulation or embryonic uterine implantation. The
CC present sequence is a target sequence from the human VEGFR2/Kdr mRNA.
XX SQ Sequence 17 BP; 5 A; 3 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 60.0%; Score 12; DB 8; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCCAGTTGAAGT 14
Db 14 CCCAGTTGAAGT 3
RESULT 159
AAT93676/c
ID AAT93676 standard; DNA; 12 BP.
XX AC AAT93676;
XX DT 26-FEB-1998 (first entry)
XX DE Exon-intron boundary of exon 8-9 of a mutant of the presenilin gene.
XX KW Presenilin gene; PS-1 gene; early-onset Alzheimers disease; polymorphism;
XX KW intron; splice site; diagnosis; beta-amyloid related disease;
XX KW PS-1 isoforms; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Mutation 6
XX FT /*tag= a
XX FT /note= "G replaced with T"
XX PN EF785282-A2.
XX PD 23-JUL-1997.
XX PF 17-JAN-1997; 97EP-00300323.
XX PR 19-JAN-1996; 96US-0010241P.
XX PA (UNIW) UNIV WASHINGTON SCHOOL MED.
XX PA (UYSP-) UNIV SOUTH FLORIDA.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.
XX PI Goate AM, Hardy JA, Roberts GW;
XX WPI; 1997-365951/34.
XX PT Detection of presenilin-1 isoforms - used for the prognosis of head-
XX PT injury subjects and the prognosis and treatment of beta-amyloid-related
XX PT diseases.
XX PS Example 3; Fig 1B; 26pp; English.
XX CC The present sequence represents part of the DNA sequence from a novel
XX CC splice mutant of the presenilin (PS-1) gene. Mutations in the PS-1 gene
XX CC on chromosome 14 have been shown to cause a significant proportion of
XX CC early-onset, autosomal dominant Alzheimers disease. Common polymorphisms
XX CC within the intron 3' to exon 9 of the PS-1 gene were identified within
XX CC and proximal to the intron. A mutation has been found in an early-onset
XX CC Alzheimers disease designated F74. This mutation is in the last
XX CC nucleotide of the intron between exons 8 and 9, where a G is replaced
XX CC with a T. This mutation spoils the the acceptor site in the middle of

CC Ser857, and is expected to alter the splicing of this region. The
 CC mutation does not change the cDNA sequence and could, therefore, only be
 CC identified by sequencing of primers derived from intronic sequences. The
 CC primers are used in a new method for diagnosing the likelihood of
 CC developing a chronic neurodegenerative pathology which could result in
 CC psychiatric or neurological disorders comprising detecting the presence or
 CC absence of PS-1 isoforms or of DNA encoding PS-1 isoforms in the subject.
 CC The methods can be used to determine the likelihood of non-response to
 CC compounds which block or alter synaptic transmission in head injuries.
 CC They can also be used for the prognosis and treatment of beta-amyloid
 CC related diseases such as early- and late-onset Alzheimer's disease,
 CC cortical Lewy body disease, Parkinson's disease and patients with
 CC vascular and cerebrovascular disease which predispose to these diseases
 XX
 SQ Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 2; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
 Db 10 GTTGATGTTG 1
 ||||| |||||

RESULT 160
 AAV42278/C
 ID AAV42278 standard; cDNA; 12 BP.

XX AC AAV42278;

XX DT 23-SEP-1998 (first entry)

XX DE Clone C1.2.1 heavy chain transcript segemnt JH.

XX KW Human; immunoglobulin; Ig; transgenic; non-human mammal;

XX KW inactivated endogenous Ig locus; B-cell development;

XX KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;

XX KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;

XX KW production; antibody; ss.

XX OS Homo sapiens.

XX FN WO9824893-A2.

XX PD 11-JUN-1998.

XX PF 03-DEC-1997; 97WO-US023091.

XX PR 03-DEC-1996; 96US-00759620.

XX PA (ABGE-) ABGENIX INC.

XX PI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;

XX DR WPI; 1998-333314/29.

XX PT New transgenic non-human mammals - having an inactivated immunoglobulin
 XX locus and a near complete human immunoglobulin locus, used for production
 XX of human antibodies.

XX PS Example 8; Page 38; 128pp; English.

XX CC AAV42252-83 represent human heavy chain immunoglobulin (Ig) transcripts
 CC expressed in Xenomouse II strains. The Xenomice were produced using the
 CC method of the invention. The specification describes a transgenic non-
 CC human mammal which has genome modifications that comprise an inactivated
 CC endogenous Ig locus, so that the mammal does not display normal B-cell
 CC development. The modified genome also has an inserted human heavy chain
 CC Ig locus in germline configuration, the human heavy chain Ig locus
 CC comprising a human micro constant region and regulatory and switch
 CC sequences, human J-H genes, human D-H genes, and human V-H genes and an

CC inserted human kappa light chain Ig locus in germline configuration, the
 CC human kappa light chain Ig locus comprising a human kappa constant
 CC region, J-kappa genes, and V-kappa genes, where the number of V-H and V-
 CC kappa genes inserted are selected to restore normal B-cell development in
 CC the mammal. The transgenic animals have a near complete human Ig locus,
 CC including both a human heavy chain locus and a human kappa light chain
 CC locus. They can be used for the production of human antibodies when
 CC exposed to particular antigens e.g. when exposed to human IL-8, EGFR or
 CC TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha
 CC respectively
 XX
 SQ Sequence 12 BP; 2 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 2; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10

Db 12 GCCCCAGTAG 3
 ||||| |||||

RESULT 161

AAV42254/C

ID AAV42254 standard; cDNA; 12 BP.

XX AC AAV42254;

XX DT 23-SEP-1998 (first entry)

XX DE Clone A2.2.1 heavy chain transcript segemnt JH.

XX KW Human; immunoglobulin; Ig; transgenic; non-human mammal;

XX KW inactivated endogenous Ig locus; B-cell development;

XX KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;

XX KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;

XX KW production; antibody; ss.

XX OS Homo sapiens.

XX PN WO9824893-A2.

XX PD 11-JUN-1998.

XX PF 03-DEC-1997; 97WO-US023091.

XX PR 03-DEC-1996; 96US-00759620.

XX PA (ABGE-) ABGENIX INC.

XX PI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;

XX DR WPI; 1998-333314/29.

XX PT New transgenic non-human mammals - having an inactivated immunoglobulin
 XX locus and a near complete human immunoglobulin locus, used for production
 XX of human antibodies.

XX PS Example 8; Page 38; 128pp; English.

XX CC AAV42252-83 represent human heavy chain immunoglobulin (Ig) transcripts
 CC expressed in Xenomouse II strains. The Xenomice were produced using the
 CC method of the invention. The specification describes a transgenic non-
 CC human mammal which has genome modifications that comprise an inactivated
 CC endogenous Ig locus, so that the mammal does not display normal B-cell
 CC development. The modified genome also has an inserted human heavy chain
 CC Ig locus in germline configuration, the human heavy chain Ig locus
 CC comprising a human micro constant region and regulatory and switch
 CC sequences, human J-H genes, human D-H genes, and human V-H genes and an
 CC inserted human kappa light chain Ig locus in germline configuration, the
 CC human kappa light chain Ig locus comprising a human kappa constant
 CC region, J-kappa genes, and V-kappa genes, where the number of V-H and V-

CC kappa genes inserted are selected to restore normal B-cell development in
 CC the mammal. The transgenic animals have a near complete human Ig locus,
 CC including both a human heavy chain locus and a human kappa light chain
 CC locus. They can be used for the production of human antibodies when
 CC exposed to particular antigens e.g. when exposed to human IL-8, EGFR or
 CC TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha
 CC respectively

XX SQ Sequence 12 BP; 2 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 2; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10

DB 12 GCCCCAGTAG 3

RESULT 162

ABH93674/C
 ID ABH93674 standard; DNA; 12 BP.

XX AC ABH93674;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 293667 for detecting SNP TSC0015722.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 293667; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15

DB 11 AGTTGAGATT 2

RESULT 163

AB102985
 ID AB102985 standard; DNA; 12 BP.

XX AC AB102985;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 302958 for detecting SNP TSC0020249.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 302958; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

DB 2 GTTGAAGATG 11

RESULT 164

AB129616
 ID AB129616 standard; DNA; 12 BP.

XX

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 285659; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 15
Db |||||
1 AGTTGAGGTT 10

RESULT 167
ABI38969
ID ABI38969 standard; DNA; 12 BP.
XX
AC ABI38969;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 338942 for detecting SNP TSC0040756.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 338942; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db |||||
1 GTTGAAGTAG 10

RESULT 168
ABH86874/C
ID ABH86874 standard; DNA; 12 BP.
XX
AC ABH86874;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 286867 for detecting SNP TSC0012861.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 286867; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;


```
Score over Length 70.0%; Pred. No. 4.4e+06; Mismatches 1; Indels 0; Gaps 0;
Best Local Similarity 90.0%;
Matches 9; Conservative 0;

QY 6 AGTTGAAGTT 15
Db 12 AGTTGAAGTT 3

RESULT 169
AB116132/c
ID AB116132 standard; DNA; 12 BP.
AC AB116132;
XX
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 316105 for detecting SNP TSC0027285.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 316105; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 170
AB154959
ID AB154959 standard; DNA; 12 BP.
AC
XX
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 343306 for detecting SNP TSC0010454.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
```

XX WO200177384-A2.
XX 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 343306; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 7 GTTGAAGTTG 16
XX DB |||||
XX 3 GTTGAAGTTG 12
XX
XX RESULT 172
XX ABH74215
XX ID ABH74215 standard; DNA; 12 BP.
XX AC ABH74215;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 274200 for detecting SNP TSC0003474.
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 274200; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 7 GTTGAAGTTG 16
XX DB |||||
XX 3 GTTGAAGTTG 12
XX
XX RESULT 173
XX ABH17933/C
XX ID ABH17933 standard; DNA; 12 BP.
XX AC ABH17933;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 317906 for detecting SNP TSC028339.
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 317906; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligomers are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | |
DB 12 AATTGAAGTT 3

RESULT 174
ABH72571/c
ID ABH72571 standard; DNA; 12 BP.

XX ABH72571;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 272556 for detecting SNP TSC0002858.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.

XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 272556; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
| | | | |
DB 2 GTAGAAGTTG 11

RESULT 176
ABI17272/c

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | |
DB 11 AGTTTAAGTT 2

RESULT 175
ABH81072
ID ABH81072 standard; DNA; 12 BP.
XX
XX ABH81072;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 281065 for detecting SNP TSC0009391.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.

XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 281065; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
| | | | |
DB 2 GTAGAAGTTG 11

```
ID  ABI117272 standard; DNA; 12 BP.
XX
AC  ABI117272;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 317245 for detecting SNP TSC0027885.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
DR  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 317245; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score Over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 6 AGTTGAAGTT 15
DB 12 AGTTTAAGTT 3
XX
RESULT 177
ABI28993/C
ID  ABI28993 standard; DNA; 12 BP.
XX
AC  ABI28993;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 328966 for detecting SNP TSC0034675.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
DR  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 317245; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score Over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 6 AGTTGAAGTT 15
DB 12 AGTTTAAGTT 3
XX
RESULT 178
ABI46836
ID  ABI46836 standard; DNA; 12 BP.
XX
AC  ABI46836;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 346809 for detecting SNP TSC0044779.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
```

```
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 346809; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 AGTTGAAGTT 15
Db |||||
2 AGTTGAAGAT 11
RESULT 179
ABH90231/C
ID ABH90231 standard; DNA; 12 BP.
XX
AC ABH90231;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 290224 for detecting SNP TSC0014248.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB0000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 290224; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 AGTTGAAGTT 15
Db |||||
2 AGTTGAAGAT 11
RESULT 180
ABI69058
ID ABI69058 standard; DNA; 12 BP.
XX
AC ABI69058;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 369031 for detecting SNP TSC0057415.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB0000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 369031; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
```

```
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db | | | | | | | |
2 GGTGAAGTTG 11

RESULT 181
ABI59044/c
ID ABI59044 standard; DNA; 12 BP.
XX
AC ABI59044;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359017 for detecting SNP TSC0051425.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 359017; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db | | | | | | | |
11 AGTTGAGTT 2

RESULT 182
ABI59044/c
ID ABI59044 standard; DNA; 12 BP.
XX
AC ABI59044;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359017 for detecting SNP TSC0051425.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 359017; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db | | | | | | | |
11 AGTTGAGTT 2

RESULT 183
ABI27390/c
ID ABI27390 standard; DNA; 12 BP.
XX
AC ABI27390;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 327363 for detecting SNP TSC0033594.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 327363; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTT 15
Db 11 AGTTTAAGTT 2
|||||
|||||
RESULT 184
ABI31330/c
ID ABI31330 standard; DNA; 12 BP.
XX AC ABI31330;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 331303 for detecting SNP TSC0036110.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 316407; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTT 15
Db 11 AGTTTAAGTT 2
|||||
|||||
RESULT 185
ABI16434
ID ABI16434 standard; DNA; 12 BP.
XX AC ABI16434;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 316407 for detecting SNP TSC0027431.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 316407; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
```

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GTTGAAGTTG 16
 |||||
 DB 1 GTTGAAGTTG 10
 |||||

RESULT 186
 ABI06955
 ID ABI06955 standard; DNA; 12 BP.
 AC ABI06955;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 DE Oligonucleotide primer SEQ ID NO 306928 for detecting SNP TSC0022250.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.

XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 306928; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15
 |||||
 DB 3 AGTTGAAGTT 12
 |||||

RESULT 187
 ABI63294
 ID ABI63294 standard; DNA; 12 BP.
 AC ABI63294;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 DE Oligonucleotide primer SEQ ID NO 363267 for detecting SNP TSC0053740.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 363267; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15
 |||||
 DB 2 AATTGAAGTT 11
 |||||

KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
PN	WO200177384-A2.
XX	
XX	18-OCT-2001.
PD	
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	
PI	Olek A, Piepenbrock C, Berlin K;
FI	
XX	
XX	WPI; 2001-657177/75.
DR	
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
XX	
XX	
PS	Claim 1; SEQ ID NO 366773; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligonucleotides are also used for detecting cell type differentiation. ABC00010
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match	42.0%; Score 8.4; DB 5; Length 12;
Score over Length	70.0%;
Best Local Similarity	90.0%; Pred. No. 4.4e+06;
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy	7 GTTGAAGTTG 16
Db	10 GTTTAAGTTG 1
RESULT 190	
ABH80048/c	
ID	ABH80048 standard; DNA; 12 BP.
XX	
AC	ABH80048;
XX	
DT	22-FEB-2002 (first entry)
XX	
DE	Oligonucleotide primer SEQ ID NO 280041 for detecting SNP TSC0008088.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
PN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
XX	

```
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 280041; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
SQ Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1

RESULT 191
ABI23882/c
ID ABI23882 standard; DNA; 12 BP.
XX
XX AC ABI23882;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 323855 for detecting SNP TSC0031647.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 292707; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
SQ Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1

RESULT 191
ABH92714/c
ID ABH92714 standard; DNA; 12 BP.
XX
XX AC ABH92714;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 292707 for detecting SNP TSC0015313.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 292707; 29pp + Sequence Listing; German.
XX
```

```
XX SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 12 GTTGAAGTTG 3

RESULT 193
AB116622/c
ID AB116622 standard; DNA; 12 BP.
XX AC AB116622;
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 316595 for detecting SNP TSC0027519.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 316595 for detecting SNP TSC0027519.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX DE Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 316595; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 11 GTTGAATTG 2

RESULT 194
AB155037
ID AB155037 standard; DNA; 12 BP.
XX AC AB155037;
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 355010 for detecting SNP TSC0049419.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX DE Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 355010; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 3 AATTGAAGTT 12

RESULT 195
AB155337/c
ID AB155337 standard; DNA; 12 BP.
XX AC AB155337;
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 355310 for detecting SNP TSC0049589.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX Central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 35310; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 11 GTTGAAGTTG 2
RESULT 196
ABH72453
ID ABH72453 standard; DNA; 12 BP.
XX AC ABH72453;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 272438 for detecting SNP TSC0002817.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW Central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
PR

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 272438; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 3 AGTTGAAGTT 12
RESULT 197
ABI33907
ID ABI33907 standard; DNA; 12 BP.
XX AC ABI33907;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 333880 for detecting SNP TSC0037804.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW Central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 333880; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP),
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 3 AGTTGAAGTT 12

RESULT 198
ABI76116
ID ABI76116 standard; DNA; 12 BP.
AC ABI76116;
XX
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 376089 for detecting SNP TSC0061604.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 376089; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 1 GTTGAAGTTG 10

RESULT 199
ABI79656/C
ID ABI79656 standard; DNA; 12 BP.
XX
XX AC ABI79656;
XX
XX 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 379629 for detecting SNP TSC0063392.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 379629; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1

```

RESULT 200
ABH95097
ID ABH95097 standard; DNA; 12 BP.
XX
XX AC ABH95097;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 295090 for detecting SNP TSC0016430.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WI PI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 274757; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 2 GTTGTAGTTG 11

RESULT 201
ABH74772/C
ID ABH74772 standard; DNA; 12 BP.
XX
XX AC ABH74772;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 274757 for detecting SNP TSC0003668.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WI PI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 295090; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 2 GTTGTAGTTG 11

RESULT 202
ABT02339
ID ABT02339 standard; DNA; 12 BP.
XX
XX AC ABT02339;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 302312 for detecting SNP TSC0019928.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WI PI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 274757; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 10 AGTCGAAGTT 1

RESULT 203
ABT02339
ID ABT02339 standard; DNA; 12 BP.
XX
XX AC ABT02339;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 302312 for detecting SNP TSC0019928.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WI PI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 274757; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 10 AGTCGAAGTT 1

```

PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 302312; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11
RESULT 203
ABI21522/C
ID ABI21522 standard; DNA; 12 BP.
XX
AC ABI21522;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 321495 for detecting SNP TSC0030284.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 321495 for detecting SNP TSC0030284.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 302312; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11
RESULT 204
ABI06231/C
ID ABI06231 standard; DNA; 12 BP.
XX
AC ABI06231;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 306204 for detecting SNP TSC0021865.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 306204; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 12 GTTGAAGTGS 3
RESULT 204
ABI06231/C
ID ABI06231 standard; DNA; 12 BP.
XX
AC ABI06231;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 306204 for detecting SNP TSC0021865.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 306204; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 12 GTTGAAGTGS 3

CC	was obtained in electronic format from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
	Query Match 42.0%; Score 8.4; DB 5; Length 12;
	Score over Length 70.0%;
	Best Local Similarity 90.0%; Pred. No. 4.4e+06;
	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	6 AGTTGAAGTT 15 12 AATTGAAGTT 3
DB	
	RESULT 205
ID	ABI10237
ID	ABI10237 standard; DNA; 12 BP.
AC	ABI10237;
DT	
DT	22-FEB-2002 (first entry)
DE	Oligonucleotide primer SEQ ID NO 310210 for detecting SNP TSC0023863.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
OS	
XX	WO200177384-A2.
PN	
XX	18-OCT-2001.
PD	
DT	22-FEB-2002 (first entry)
DE	Oligonucleotide primer SEQ ID NO 347105 for detecting SNP TSC0044912.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
OS	
XX	WO200177384-A2.
PN	
XX	18-OCT-2001.
PD	
DT	06-APR-2001; 2001WO-IB000713.
DE	Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX	Claim 1; SEQ ID NO 347105; 29pp + Sequence Listing; German.
PS	
XX	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC	
XX	Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
	Query Match 42.0%; Score 8.4; DB 5; Length 12;
	Score over Length 70.0%;
	Best Local Similarity 90.0%; Pred. No. 4.4e+06;
	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	6 AGTTGAAGTT 15 11 AGTTAAAGTT 2
DB	
	RESULT 207
ID	ABH96302/c
ID	ABH96302 standard; DNA; 12 BP.
AC	ABH96302;
DT	
DT	22-FEB-2002 (first entry)
DE	Oligonucleotide primer SEQ ID NO 296295 for detecting SNP TSC0017012.


```
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 296295; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGTT 15
XX ||| |||||
XX 12 AGTAGAAGTT 3
XX
XX RESULT 208
XX ABI06525
XX ID ABI06525 standard; DNA; 12 BP.
XX
XX AC ABI06525;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 306498 for detecting SNP TSC0022053.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
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XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 306498; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGTT 15
XX ||| |||||
XX 2 AGTTAAAGTT 11
XX
XX Db
XX
XX RESULT 209
XX ABI31606/C
XX ID ABI31606 standard; DNA; 12 BP.
XX
XX AC ABI31606;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 331579 for detecting SNP TSC0036328.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
```

XX PS Claim 1; SEQ ID NO 331579; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH9989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

RESULT 210
ABI31734/c
ID ABI31734 standard; DNA; 12 BP.

XX AC ABI31734;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 331707 for detecting SNP TSC0036424.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX Claim 1; SEQ ID NO 331707; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH9989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

RESULT 210
ABI31734/c
ID ABI31734 standard; DNA; 12 BP.

XX AC ABI31734;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 331707 for detecting SNP TSC0036424.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX Claim 1; SEQ ID NO 331707; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH9989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

RESULT 211
ABI43151
ID ABI43151 standard; DNA; 12 BP.

XX AC ABI43151;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 343124 for detecting SNP TSC0042902.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX Claim 1; SEQ ID NO 343124; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH9989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

CC data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

RESULT 211
ABI43151
ID ABI43151 standard; DNA; 12 BP.

XX AC ABI43151;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 343124 for detecting SNP TSC0042902.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX Claim 1; SEQ ID NO 343124; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH9989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

```
Db      ||||| |||||
        2 AGTTAAGTT 11

RESULT 212
AB136211/c
ID AB136211 standard; DNA; 12 BP.
XX
XX
AC AB136211;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 336184 for detecting SNP TSC0039238.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EP1G-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 336184; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GTTGAAGTTG 16
Db 12 GTTGTAGTTG 3

RESULT 213
AB159670
ID AB159670 standard; DNA; 12 BP.
XX
XX AB159670;
AC AB159670;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 371399 for detecting SNP TSC0058753.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EP1G-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 336184; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15
Db 1 AGTTGAGGTT 10

RESULT 214
AB171426
ID AB171426 standard; DNA; 12 BP.
XX
XX AB171426;
AC AB171426;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 371399 for detecting SNP TSC0058753.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
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PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 371399; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
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CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10
RESULT 215
ABI69057
ID ABI69057 standard; DNA; 12 BP.
XX
AC ABI69057;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 369030 for detecting SNP TSC0057415.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 371399; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10
RESULT 216
ABI63702
ID ABI63702 standard; DNA; 12 BP.
XX
AC ABI63702;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 363675 for detecting SNP TSC0053997.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 363675; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
DB 2 GTTGAAGTTG 11
RESULT 216
ABI63702
ID ABI63702 standard; DNA; 12 BP.
XX
AC ABI63702;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 363675 for detecting SNP TSC0053997.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 363675; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
DB 2 GTTGAAGTTG 11

```

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 AAGTGGCGT 20

Db 3 AAGTGTCT 12

RESULT 217

ABH93128/c
ID ABH93128 standard; DNA; 12 BP.

XX AC ABH93128;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 293121 for detecting SNP TSC0015507.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 293121; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15

Db 12 AGTTGGAGTT 3

RESULT 218

ABH69605/c
ID ABH69605 standard; DNA; 12 BP.

XX AC ABH69605;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 269582 for detecting SNP TSC0001812.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 269582; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15

Db 10 AGTTGGAGTT 1

RESULT 219

ABI23801/c
ID ABI23801 standard; DNA; 12 BP.

XX AC ABI23801;

XX DT 22-FEB-2002 (first entry)

```
XX DE Oligonucleotide primer SEQ ID NO 323774 for detecting SNP TSC0031607.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 323774; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIO0010-ABIO2073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTT 15
XX DB | | | | | | |
XX 12 ATTTGAAGTT 3
XX RESULT 220
XX ABH70890/C
XX ID ABH70890 standard; DNA; 12 BP.
XX AC ABH70890;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 270867 for detecting SNP TSC0002305.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 323774; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIO0010-ABIO2073
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XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTT 15
XX DB | | | | | | |
XX 12 ATTTGAAGTT 3
XX RESULT 220
XX ABH70890/C
XX ID ABH70890 standard; DNA; 12 BP.
XX AC ABH70890;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 329753 for detecting SNP TSC0035126.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 270867; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIO0010-ABIO2073
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XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTT 15
XX DB | | | | | | |
XX 10 AGTTGAAGTT 1
XX RESULT 221
XX ABI29780
XX ID ABI29780 standard; DNA; 12 BP.
XX AC ABI29780;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 329753 for detecting SNP TSC0035126.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
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PT methylation status.
XX Claim 1; SEQ ID NO 270867; 29pp + Sequence Listing; German.
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XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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XX central nervous system, cardiovascular and metabolic disorders. The
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XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIO0010-ABIO2073
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```

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 329753; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
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CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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CC data for this patent did not form part of the printed specification, but
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XX Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

|||||
Db 3 GTTGAAGTTG 12

RESULT 222

ABI12820

ID ABI12820 standard; DNA; 12 BP.

AC ABI12820;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 312793 for detecting SNP TSC0025301.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 312793; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

|||||
Db 2 GTTGAAGTTG 11

RESULT 223

ABI47302

ID ABI47302 standard; DNA; 12 BP.

XX

AC ABI47302;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 347275 for detecting SNP TSC0045008.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 347275; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      6 AGTTGAAGTT 15
Db      |||||
        2 AGTTAAAGTT 11

RESULT 224
ABI41710
ID      ABI41710 standard; DNA; 12 BP.
XX
AC      ABI41710;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 341683 for detecting SNP TSC0042183.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PP      07-APR-2000; 2000DE-01019173.
XX
PS      Claim 1; SEQ ID NO 341683; 29pp + Sequence Listing; German.
XX
PA      (EPIC-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 341683; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match      42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      |||||
        2 GTTGAAGTTG 11

RESULT 225
ABI75716
ID      ABI75716 standard; DNA; 12 BP.
XX
AC      ABI75716;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 293477 for detecting SNP TSC0015632.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PP      07-APR-2000; 2000DE-01019173.
XX
PS      Claim 1; SEQ ID NO 375689; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match      42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      |||||
        2 AGTTGAAGTT 11

RESULT 226
ABH93484/C
ID      ABH93484 standard; DNA; 12 BP.
XX
AC      ABH93484;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 293477 for detecting SNP TSC0015632.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX

```


CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15
 |||||
 DB 3 AGTTGAAGTT 12
 |||||

RESULT 229
 ABH81937/c
 ID ABH81937 standard; DNA; 12 BP.

XX ABH81937;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 281930 for detecting SNP TSC0010165.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 281930; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 7 GTTGAAGTTG 16
 |||||
 DB 11 GTTGTAGTTG 2
 |||||

RESULT 230

ABI73613
 ID ABI73613 standard; DNA; 12 BP.

XX ABI73613;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 373586 for detecting SNP TSC0060183.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 373586; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15
 |||||

DB 1 AGTTGTAGTT 10
 |||||

RESULT 231

ABI53913/c
 ID ABI53913 standard; DNA; 12 BP.

XX ABI53913;

```
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 353886 for detecting SNP TSC0048785.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 300438; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGTT 15
XX DB 12 AGTTGAAGAT 3
XX
XX RESULT 232
XX ID ABI00465 standard; DNA; 12 BP.
XX AC ABI00465;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 300438 for detecting SNP TSC0019035.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 353886; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGTT 15
XX DB 12 AGTTGAAGAT 3
XX
XX RESULT 233
XX ID ABH99246 standard; DNA; 12 BP.
XX AC ABH99246;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 299239 for detecting SNP TSC0018492.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX
```

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 299239; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
6 AGTTGAAGTTG 15
3 ATTTGAAGTTG 12
RESULT 234
ABH88414/c
ID ABH88414 standard; DNA; 12 BP.
XX
AC ABH88414;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 288407 for detecting SNP TSC0013497.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 288407; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
7 GTTGAAGTTG 16
12 GTTAAAGTTG 3
RESULT 235
ABI66132/c
ID ABI66132 standard; DNA; 12 BP.
XX
AC ABI66132;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 366105 for detecting SNP TSC0010825.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 366105; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;

```
Best Local Similarity 90.0%; Pred. No. 4.4e+06; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTGAAGTT 2

RESULT 236
ABI67005/c
ID ABI67005 standard; DNA; 12 BP.
XX AC ABI67005;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 366978 for detecting SNP TSC0056077.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 366978; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAAGTTG 3

RESULT 237
ABI67274
ID ABI67274 standard; DNA; 12 BP.
XX AC ABI67274;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352722 for detecting SNP TSC0048058.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 366978; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 1 AGTGAAGTT 10

RESULT 238
ABI52749
ID ABI52749 standard; DNA; 12 BP.
XX AC ABI52749;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352722 for detecting SNP TSC0048058.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 367247; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 1 AGTGAAGTT 10

RESULT 238
ABI52749
ID ABI52749 standard; DNA; 12 BP.
XX AC ABI52749;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352722 for detecting SNP TSC0048058.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 367247; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
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PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 316596; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 7 GTTGAAGTTG 16
DB 2 GTTTAAGTTG 11
XX
RESULT 239
AB116623/C
ID AB116623 standard; DNA; 12 BP.
XX
AC AB116623;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 316596 for detecting SNP TSC0027519.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 352722; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 7 GTTGAAGTTG 16
DB 2 GTTTAAGTTG 11
XX
RESULT 240
AB144330
ID AB144330 standard; DNA; 12 BP.
XX
AC AB144330;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 344303 for detecting SNP TSC0043488.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 344303; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 7 GTTGAAGTTG 16
DB 11 GTTGAATTTG 2
XX
RESULT 240
AB144330
ID AB144330 standard; DNA; 12 BP.
XX
AC AB144330;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 344303 for detecting SNP TSC0043488.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 344303; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
```

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11
|||||

RESULT 241
ABI61490
ID ABI61490 standard; DNA; 12 BP.

XX ABI61490;

AC 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 361463 for detecting SNP TSC0052647.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 361463; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 3 AGTTGAAGTT 12
|||||

RESULT 242

ABI74887

ID ABI74887 standard; DNA; 12 BP.

XX ABI74887;

AC 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 374860 for detecting SNP TSC0060940.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 374860; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 2 GTTGAAGTTG 11
|||||

RESULT 243

ABI10236

ID ABI10236 standard; DNA; 12 BP.

```
XX AC ABI10236;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 310209 for detecting SNP TSC0023863.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 310209; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 7 GTTGAAGTTG 16
XX DB 1 GTTGAAGTTG 10
XX
XX RESULT 244
XX ABI1459/C
XX ID ABI1459 standard; DNA; 12 BP.
XX AC ABI1459;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 31432 for detecting SNP TSC0036202.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 31432; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 7 GTTGAAGTTG 16
XX DB 1 GTTGAAGTTG 10
XX
XX RESULT 244
XX ABI1459/C
XX ID ABI1459 standard; DNA; 12 BP.
XX AC ABI1459;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 31432 for detecting SNP TSC0036202.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 31432; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 7 GTTGAAGTTG 16
XX DB 12 GTTGAAGTTG 3
XX
XX RESULT 245
XX ABI32242/C
XX ID ABI32242 standard; DNA; 12 BP.
XX AC ABI32242;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 332215 for detecting SNP TSC0036773.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
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XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 332215; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGTT 2
RESULT 246
ABI69897
ID ABI69897 standard; DNA; 12 BP.
XX
AC ABI69897;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 369870 for detecting SNP TSC0057857.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 369870; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGTT 2

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10
RESULT 247
ABH92665/c
ID ABH92665 standard; DNA; 12 BP.
XX
AC ABH92665;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 292658 for detecting SNP TSC0015297.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 292658; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

```
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGAT 2

RESULT 248
ABI29165/c
ID ABI29165 standard; DNA; 12 BP.
XX
AC ABI29165;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329138 for detecting SNP TSC0034774.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 329138; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1

RESULT 249
ABI22105/c
ID ABI22105 standard; DNA; 12 BP.
XX
AC ABI22105;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322078 for detecting SNP TSC0030647.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 322078; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1

RESULT 250
ABH97330
ID ABH97330 standard; DNA; 12 BP.
XX
AC ABH97330;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 297323 for detecting SNP TSC0017523.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

```
OS Homo sapiens.
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 297323; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB ||||| |||||
2 AGTTGAGTT 11
RESULT 251
ABI02630/C
ID ABI02630 standard; DNA; 12 BP.
XX
XX ABI02630;
AC
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 302603 for detecting SNP TSC0020078.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 297323; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB ||||| |||||
2 AGTTGAGTT 11
RESULT 252
ABH84497
ID ABH84497 standard; DNA; 12 BP.
XX
XX ABH84497;
AC
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 284490 for detecting SNP TSC0011855.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 284490; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
```

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
 Db 2 AGTGAAGTT 11

RESULT 253
 ABI38801/c
 ID ABI38801 standard; DNA; 12 BP.

XX ABI38801;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 338774 for detecting SNP TSC0040669.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 338774; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
 Db 10 ATTTGAAGTT 1

RESULT 254
 ABI62796/c
 ID ABI62796 standard; DNA; 12 BP.

XX ABI62796;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 362769 for detecting SNP TSC0053437.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 362769; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
 Db 10 AGATGAAGTT 1

RESULT 255

AB164102
ID AB164102 standard; DNA; 12 BP.
XX AC
XX AC AB164102;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide primer SEQ ID NO 364075 for detecting SNP TSC0054253.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
OS Homo sapiens.
XX XX
PN WO200177384-A2.
XX XX
PD 18-OCT-2001.
XX XX
PF 06-APR-2001; 2001WO-IB000713.
XX XX
PR 07-APR-2000; 2000DE-01019173.
XX XX
PA (EPIG-) EPIGENOMICS AG.
XX XX
PI Olek A, Piepenbrock C, Berlin K;
XX XX
DR WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
PS Claim 1; SEQ ID NO 364075; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ASC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 6 AGTTGAAGTT 15
DB 1 AGTTGTAGTT 10
|||||
|||||

RESULT 256
ABH92662/C
ID ABH92662 standard; DNA; 12 BP.
XX AC
XX AC ABH92662;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide primer SEQ ID NO 292655 for detecting SNP TSC0015296.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX

XX	Homo sapiens.
OS	WO200177384-A2.
XX	18-OCT-2001.
XX	06-APR-2001; 2001WO-IB000713.
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
XX	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2001-657177/75.
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX	Claim 1; SEQ ID NO 292655; 29pp + Sequence Listing; German.
XX	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
XX	Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX	Score over Length 70.0%;
XX	Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	6 AGTTGAAGTT 15
Db	
	12 AGTTGAAGTT 3
RESULT 257	
ABI18502/c	
ID	ABI18502 standard; DNA; 12 BP.
XX	ABI18502;
AC	
XX	22-FEB-2002 (first entry)
DT	
DE	Oligonucleotide primer SEQ ID NO 318475 for detecting SNP TSC0028677.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
OS	WO200177384-A2.
XX	18-OCT-2001.
XX	06-APR-2001; 2001WO-IB000713.
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 318475; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1
RESULT 258
ABI47133/C
ID ABI47133 standard; DNA; 12 BP.
XX
AC ABI47133;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 347106 for detecting SNP TSC0044912.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 347106; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 11 AGTTGAAGTT 2
RESULT 259
ABI41721/C
ID ABI41721 standard; DNA; 12 BP.
XX
AC ABI41721;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 341694 for detecting SNP TSC0042185.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 341694; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

```
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 10 GTTGAGGTG 1

RESULT 260
ABI42212/c
ID ABI42212 standard; DNA; 12 BP.
XX AC ABI42212;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 342185 for detecting SNP TSC0042419.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WO200177384-A2.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 342185; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 11 AGTTAAAGTT 2

RESULT 262
ABI67350/c
ID ABI67350 standard; DNA; 12 BP.
XX AC ABI67350;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 367323 for detecting SNP TSC0009154.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```


CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGAT 2
|||||||

RESULT 265
ABH95291
ID ABH95291 standard; DNA; 12 BP.
AC ABH95291;
XX
XX 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 295284 for detecting SNP TSC0016521.
KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
PD 18-OCT-2001.
PF
PP 06-APR-2001; 2001WO-IB000713.
PR 07-APR-2000; 2000DE-01019173.
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 295284; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGAT 2
|||||||

RESULT 265
ABH95291
ID ABH95291 standard; DNA; 12 BP.
AC ABH95291;
XX
XX 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 295284 for detecting SNP TSC0016521.
KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
PD 18-OCT-2001.
PF
PP 06-APR-2001; 2001WO-IB000713.
PR 07-APR-2000; 2000DE-01019173.
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 295284; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 3 AGTTGAAGTT 12
|||||||

RESULT 266
ABH98049
ID ABH98049 standard; DNA; 12 BP.
AC ABH98049;
XX
XX 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 298042 for detecting SNP TSC0017887.
KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
PD 18-OCT-2001.
PF
PP 06-APR-2001; 2001WO-IB000713.
PR 07-APR-2000; 2000DE-01019173.
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 298042; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 3 GTTGAAGTTG 12
|||||||

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RESULT 267
ABI33882/c
ID ABI33882 standard; DNA; 12 BP.
XX
AC ABI33882;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 333855 for detecting SNP TSC0037792.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 333855; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGTT 2
RESULT 268
ABI41817/c
ID ABI41817 standard; DNA; 12 BP.
XX
AC ABI41817;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 341790 for detecting SNP TSC0042229.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 341790; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
DB 12 GTTGAAGTTG 3
RESULT 269
ABI48505/c
ID ABI48505 standard; DNA; 12 BP.
XX
AC ABI48505;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 348478 for detecting SNP TSC0045610.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
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XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 348478; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 ATTGAAGTT 2
|||||
11 AGTTGAAGTT 2

RESULT 270
ABI76925/c
ID ABI76925 standard; DNA; 12 BP.
XX AC ABI76925;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 376898 for detecting SNP TSC0062033.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 376898; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGAAGTT 2
|||||
11 AGTTGAAGTT 2

RESULT 271
ABI72013
ID ABI72013 standard; DNA; 12 BP.
XX AC ABI72013;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 371986 for detecting SNP TSC0059100.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 371986; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
```


KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 364597; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 12 GATGAAGTTG 3
RESULT 275
ABI62006/C
ID ABI62006 standard; DNA; 12 BP.
AC ABI62006;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 361979 for detecting SNP TSC0052975.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX

PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 361979; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 12 AGTTGAAGTT 3
RESULT 276
ABI17895/C
ID ABI17895 standard; DNA; 12 BP.
XX
AC ABI17895;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 317868 for detecting SNP TSC0028311.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

PS Claim 1; SEQ ID NO 317868; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 ATTGAAGTT 2

RESULT 277
ABH94593/c
ID ABH94593 standard; DNA; 12 BP.

XX ABH94593;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 294586 for detecting SNP TSC0016192.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 294586; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 ATTGAAGTT 2

RESULT 277
ABH94593/c
ID ABH94593 standard; DNA; 12 BP.

XX ABH94593;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 294586 for detecting SNP TSC0016192.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 294586; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 ATTGAAGTT 2

RESULT 278
ABH96494
ID ABH96494 standard; DNA; 12 BP.

XX ABH96494;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 296487 for detecting SNP TSC0017101.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 296487; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 ATTGAAGTT 2

Db 3 AGTAGAAGTT 12

RESULT 279
ABI39317
ID ABI39317 standard; DNA; 12 BP.
XX
AC ABI39317;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 339290 for detecting SNP TSC0007278.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 339290; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 2 AGTTGAATTT 11
RESULT 280
ABI52789/c
ID ABI52789 standard; DNA; 12 BP.
XX
AC ABI52789;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 352762 for detecting SNP TSC0048084.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 352762; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 10 AGTTGTAGTT 1
RESULT 281
ABI47624/c
ID ABI47624 standard; DNA; 12 BP.
XX
AC ABI47624;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 347597 for detecting SNP TSC0045181.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.
 XX (EPIC-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 347597; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 GTTGAAGTTG 16
 Db 11 GTTGAATTG 2
 RESULT 282
 ABI77409/c
 ID ABI77409 standard; DNA; 12 BP.
 XX AC ABI77409;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 377382 for detecting SNP TSC0062298.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIC-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 377382; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 5; Length 12;
 Score over Length 70.0%;
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 6 AGTTGAAGTT 15
 Db 11 AATTGAAGTT 2
 RESULT 283
 ADD69888/c
 ID ADD69888 standard; DNA; 12 BP.
 XX AC ADD69888;
 XX 15-JAN-2004 (first entry)
 DT Let-7 L6 loop DNA.
 DE down-regulation; RNA degradation; toxic protein knock-down;
 KW virus production; GL2; Let-7; GL3; ds.
 XX Unidentified.
 OS WO2003020931-A2.
 PN 13-MAR-2003.
 PD 29-AUG-2002; 2002WO-EP009670.
 PF 01-SEP-2001; 2001US-0317229P.
 PR 04-JUN-2002; 2002US-0385733P.
 XX (GALA-) GALAPAGOS GENOMICS NV.
 PA Arts G, Langemeijer EV, Piest I, Van Es HHG, Michiels GAM;
 PI WPI; 2003-290193/28.
 DR Novel polynucleotide useful for down regulation or degradation of
 PT specific RNA molecule in host cell, has sequence complementary to host
 PT RNA sequence and linked to a sequence capable of forming stem-loop
 PT structure.
 XX Example 2; Fig 11; 166pp; English.
 PS The invention relates to a novel isolated polynucleotide useful for the
 CC down-regulation or degradation of a specific RNA molecule in a host cell
 CC comprising a first polynucleotide sequence complementary to the RNA
 CC sequence in the host cell, covalently linked to a second RNA sequence
 CC capable of forming a stem-loop structure where the first polynucleotide
 CC is an RNA sequence or a single-stranded DNA equivalent. The
 CC polynucleotide of the invention may be useful for the down regulation or
 CC degradation of a specific RNA molecule in a host cell, for producing

CC viral vectors encoding a toxic protein, for treatment in a human or
CC animal and for temporary knock-down of proteins, such as lethal proteins,
CC during virus production. The current sequence is that of the Let-7 loop
CC DNA of the invention.

XX SQ Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 8; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 12
| | | | | | | |
Db 10 CCCAGTTCAA 1

RESULT 284
AER38463/C
ID AER38463 standard; DNA; 12 BP.

XX AC AER38463;

XX DT 05-APR-2007 (first entry)

XX DE Lipid metabolism protein (LMP) related DNA SEQ ID NO:132.

XX KW Genetic engineering; plant growth regulation; gene expression; seed;
KW lipid metabolism protein; LMP; transgenic plant; oil; drought tolerance;
KW cold tolerance; plant; ds.

XX OS Synthetic.
OS Unidentified.

XX FN WO2007012576-A2.

XX PD 01-FEB-2007.

XX PF 14-JUL-2006; 2006WO-EP064276.

XX PR 25-JUL-2005; 2005US-0595649P.

XX PA (BADI) BASF PLANT SCI.

XX PI Zank T, Oswald O;

XX DR WPI; 2007-176883/17.

XX PT New isolated lipid metabolism protein polynucleotides and polypeptides,
PT useful for stimulating or modulating plant growth and plant yield, e.g.
PT increasing plant growth under adverse conditions of drought, cold, or
PT light.

XX PS Claim 6; SEQ ID NO 132; 128pp; English.

XX CC The invention relates to an isolated nucleic acid comprising two or more
CC lipid metabolism protein (LMP) polynucleotide sequences encoding LMP
CC polypeptides. The invention also relates to an expression vector
CC containing the nucleic acid, where the nucleic acid is operatively linked
CC to a promoter selected from a seed-specific promoter, a root-specific
CC promoter or a non-tissue-specific promoter, a method of producing a
CC transgenic plant having a modified level of a seed storage compound
CC weight percentage compared to an empty vector control, a method of
CC modulating the level of a seed storage compound weight percentage in a
CC plant comprising modifying the expression of a nucleic acid in the plant,
CC a transgenic plant made by the method and a seed produced by the
CC transgenic plant, where the plant expresses the polypeptide that
CC functions as a modulator of a seed storage compound and where the plant
CC is true breeding for a modified level of seed storage compound weight
CC percentage as compared to an empty vector control. The polynucleotides
CC and polypeptides are useful for producing transgenic plants with improved
CC quality traits, for manipulating fatty acid-related compounds, for
CC increasing oil levels and for altering the fatty acid composition in

CC plants and seeds. The sequences are also useful for stimulating or
CC modulating plant growth and plant yield, preferably for increasing plant
CC growth under adverse conditions (e.g. drought, cold, light, UV) and for
CC improving seed germination and seed dormancy, thus improving plant growth
CC and/or yield of seed storage compounds. This sequence represents LMP
CC related DNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 12 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 2 Other;

Query Match 42.0%; Score 8.4; DB 22; Length 12;
Score over Length 70.0%;
Best Local Similarity 75.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
| | | | | | | |
Db 12 AGYTGASGTGGC 1

Search completed: December 4, 2007, 01:29:56
Job time : 474 secs

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 17:15:22 ; Search time 17683 seconds
(without alignments)
74.102 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagtggaagtgccgt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 93186685 seqs, 32758818645 residues

Total number of hits satisfying chosen parameters: 1276

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum score over Length 70%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Score Length	Query Match	Length	ID	Description
1	20	100.0	100.0	20	1	PCT-US02-22417-64
2	20	100.0	100.0	20	34	US-09-908-147-64
3	20	100.0	100.0	20	56	US-10-728-509-64
4	18	90.0	90.0	20	1	PCT-US02-22417-65
5	18	90.0	90.0	20	34	US-09-908-147-65
6	18	90.0	90.0	20	56	US-10-728-509-65
7	11.4	87.7	57.0	13	52	US-10-708-953-393940
8	11.4	87.7	57.0	13	52	US-10-708-953-423956
9	11.4	87.7	57.0	13	52	US-10-708-953-580710
10	11.4	87.7	57.0	13	52	US-10-708-953-801440
11	11.4	87.7	57.0	13	52	US-10-708-953-1058146
12	11.4	87.7	57.0	13	52	US-10-708-953-1198625

13	11.4	87.7	57.0	13	52	US-10-708-953-2178793	Sequence 2	C 86	12	80.0	60.0	15	33	US-09-870-161-4126	Sequence 4
14	11.4	87.7	57.0	13	53	US-10-708-953A-393940	Sequence 3	C 87	12	80.0	60.0	15	41	US-10-287-949A-4126	Sequence 4
15	11.4	87.7	57.0	13	53	US-10-708-953A-423956	Sequence 4	C 88	12	80.0	60.0	15	41	US-10-287-949B-4126	Sequence 4
16	11.4	87.7	57.0	13	53	US-10-708-953A-580710	Sequence 5	C 89	12	80.0	60.0	15	41	US-10-287-949C-4126	Sequence 4
17	11.4	87.7	57.0	13	53	US-10-708-953A-801440	Sequence 8	C 90	12	80.0	60.0	15	41	US-10-294-038-5264	Sequence 5
18	11.4	87.7	57.0	13	53	US-10-708-953A-1058146	Sequence 1	C 91	12	80.0	60.0	15	41	US-10-294-038A-5264	Sequence 5
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84	16	80.0	80.0	20	48	US-10-594-448-16	Sequence 1	C 157	12.4	77.5	62.0	16	46	US-10-367-832A-54229	Sequence 5
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c 167	10.8	77.1	54.0	14	52	US-10-708-953-2077386	Sequence 2	c 240	9.8	75.4	49.0	13	52	US-10-708-953-2083562	Sequence 2
c 168	10.8	77.1	54.0	14	53	US-10-708-953A-528084	Sequence 5	c 241	9.8	75.4	49.0	13	52	US-10-708-953-2156300	Sequence 2
c 169	10.8	77.1	54.0	14	53	US-10-708-953A-613923	Sequence 6	c 242	9.8	75.4	49.0	13	52	US-10-708-953-2181596	Sequence 2
c 170	10.8	77.1	54.0	14	53	US-10-708-953A-668724	Sequence 6	c 243	9.8	75.4	49.0	13	53	US-10-708-953A-151962	Sequence 5
c 171	10.8	77.1	54.0	14	53	US-10-708-953A-1269719	Sequence 1	c 244	9.8	75.4	49.0	13	53	US-10-708-953A-683001	Sequence 6
c 172	10.8	77.1	54.0	14	53	US-10-708-953A-1475347	Sequence 1	c 245	9.8	75.4	49.0	13	53	US-10-708-953A-755878	Sequence 7
c 173	10.8	77.1	54.0	14	53	US-10-708-953A-1713144	Sequence 1	c 246	9.8	75.4	49.0	13	53	US-10-708-953A-804357	Sequence 8
c 174	10.8	77.1	54.0	14	53	US-10-708-953A-1883139	Sequence 1	c 247	9.8	75.4	49.0	13	53	US-10-708-953A-840357	Sequence 9
c 175	10.8	77.1	54.0	14	53	US-10-708-953A-1898598	Sequence 1	c 248	9.8	75.4	49.0	13	53	US-10-708-953A-1014267	Sequence 1
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c 177	10.8	77.1	54.0	14	53	US-10-709-572-163869	Sequence 1	c 250	9.8	75.4	49.0	13	53	US-10-708-953A-1151132	Sequence 1
c 178	10.8	77.1	54.0	14	53	US-10-709-572-191117	Sequence 1	c 251	9.8	75.4	49.0	13	53	US-10-708-953A-1169509	Sequence 1
c 179	10.8	77.1	54.0	14	53	US-10-709-572-191263	Sequence 2	c 252	9.8	75.4	49.0	13	53	US-10-708-953A-1571840	Sequence 1
c 180	10.8	77.1	54.0	14	53	PCT-US04-02720-1484	Sequence 2	c 253	9.8	75.4	49.0	13	53	US-10-708-953A-1618678	Sequence 1
c 181	10.8	76.9	50.0	13	24	US-09-528-209A-6286	Sequence 1	c 254	9.8	75.4	49.0	13	53	US-10-708-953A-1873083	Sequence 1
c 182	10.8	76.9	50.0	13	24	US-10-051-645B-5965	Sequence 6	c 255	9.8	75.4	49.0	13	53	US-10-708-953A-2013164	Sequence 1
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c 184	10.8	76.9	50.0	13	40	US-10-257-017B-28743	Sequence 2	c 257	9.8	75.4	49.0	13	53	US-10-708-953A-2156300	Sequence 2
c 185	10.8	76.9	50.0	13	40	US-10-257-017B-28744	Sequence 2	c 258	9.8	75.4	49.0	13	53	US-10-708-953A-2181596	Sequence 2
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c 188	10.8	76.9	50.0	13	40	US-10-257-017B-107775	Sequence 1	c 261	12.8	75.3	64.0	17	3	PCT-US06-29646A-101428	Sequence 1
c 189	10.8	76.9	50.0	13	40	US-10-257-017B-107775	Sequence 1	c 262	12.8	75.3	64.0	17	48	US-10-533-164-454911	Sequence 4
c 190	10.8	76.9	50.0	13	40	US-10-257-017B-131257	Sequence 1	c 263	12.8	75.3	64.0	17	48	US-10-603-923-625220	Sequence 6
c 191	10.8	76.9	50.0	13	40	US-10-257-017B-131257	Sequence 1	c 264	12.8	75.3	64.0	17	51	US-10-707-975B-497939	Sequence 4
c 192	10.8	76.9	50.0	13	40	US-10-257-017B-150111	Sequence 1	c 265	12.8	75.3	64.0	17	77	US-11-495-951A-101428	Sequence 1
c 193	10.8	76.9	50.0	13	40	US-10-257-017B-150112	Sequence 1	c 266	12.8	75.3	64.0	16	52	US-10-708-953-1313224	Sequence 1
c 194	10.8	76.9	50.0	13	40	US-10-257-017B-153411	Sequence 1	c 267	12.8	75.3	64.0	16	52	US-10-708-953-1313224	Sequence 1
c 195	10.8	76.9	50.0	13	40	US-10-257-017B-153412	Sequence 1	c 268	12.8	75.3	64.0	16	53	US-10-708-953A-1313224	Sequence 1
c 196	10.8	76.9	50.0	13	40	US-10-257-017B-171651	Sequence 1	c 269	12.8	75.3	64.0	16	53	US-10-708-953A-1811627	Sequence 1
c 197	10.8	76.9	50.0	13	40	US-10-257-017B-171652	Sequence 1	c 270	9.75	45.0	45.0	12	40	US-10-257-017B-272526	Sequence 2
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c 199	10.8	76.9	50.0	13	62	US-11-051-720-809	Sequence 8	c 272	9.75	45.0	45.0	12	40	US-10-257-017B-284630	Sequence 2
c 200	10.8	76.9	50.0	13	81	US-11-711-827-704	Sequence 7	c 273	9.75	45.0	45.0	12	40	US-10-257-017B-288152	Sequence 2
c 201	11.4	76.0	57.0	15	1	PCT-US02-25943-11543	Sequence 1	c 274	9.75	45.0	45.0	12	40	US-10-257-017B-298602	Sequence 2
c 202	11.4	76.0	57.0	15	40	US-10-227-565-11543	Sequence 1	c 275	9.75	45.0	45.0	12	40	US-10-257-017B-298745	Sequence 2
c 203	11.4	76.0	57.0	15	41	US-10-239-054A-10916	Sequence 1	c 276	9.75	45.0	45.0	12	40	US-10-257-017B-299931	Sequence 2
c 204	11.4	76.0	57.0	15	46	US-10-367-832A-11543	Sequence 1	c 277	9.75	45.0	45.0	12	40	US-10-257-017B-303341	Sequence 3
c 205	11.4	76.0	57.0	15	52	US-10-708-953-383591	Sequence 3	c 278	9.75	45.0	45.0	12	40	US-10-257-017B-305026	Sequence 3
c 206	11.4	76.0	57.0	15	52	US-10-708-953-409578	Sequence 4	c 279	9.75	45.0	45.0	12	40	US-10-257-017B-307994	Sequence 3
c 207	11.4	76.0	57.0	15	52	US-10-708-953-572403	Sequence 5	c 280	9.75	45.0	45.0	12	40	US-10-257-017B-310012	Sequence 3
c 208	11.4	76.0	57.0	15	52	US-10-708-953-716806	Sequence 7	c 281	9.75	45.0	45.0	12	40	US-10-257-017B-319646	Sequence 3
c 209	11.4	76.0	57.0	15	52	US-10-708-953-1012891	Sequence 1	c 282	9.75	45.0	45.0	12	40	US-10-257-017B-32564	Sequence 3
c 210	11.4	76.0	57.0	15	52	US-10-708-953-1276947	Sequence 1	c 283	9.75	45.0	45.0	12	40	US-10-257-017B-332564	Sequence 3
c 211	11.4	76.0	57.0	15	52	US-10-708-953-1931848	Sequence 1	c 284	9.75	45.0	45.0	12	40	US-10-257-017B-333972	Sequence 3
c 212	11.4	76.0	57.0	15	53	US-10-708-953A-383591	Sequence 3	c 285	9.75	45.0	45.0	12	40	US-10-257-017B-337673	Sequence 3
c 213	11.4	76.0	57.0	15	53	US-10-708-953A-409578	Sequence 4	c 286	9.75	45.0	45.0	12	40	US-10-257-017B-338530	Sequence 3
c 214	11.4	76.0	57.0	15	53	US-10-708-953A-572403	Sequence 5	c 287	9.75	45.0	45.0	12	40	US-10-257-017B-338626	Sequence 3
c 215	11.4	76.0	57.0	15	53	US-10-708-953A-716806	Sequence 7	c 288	9.75	45.0	45.0	12	40	US-10-257-017B-342781	Sequence 3
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c 217	11.4	76.0	57.0	15	53	US-10-708-953A-1276947	Sequence 1	c 290	9.75	45.0	45.0	12	40	US-10-257-017B-345821	Sequence 3
c 218	11.4	76.0	57.0	15	53	US-10-708-953A-1931848	Sequence 1	c 291	9.75	45.0	45.0	12	40	US-10-257-017B-358109	Sequence 3
c 219	9.8	75.4	49.0	13	51	US-10-708-952A-102785	Sequence 1	c 292	9.75	45.0	45.0	12	40	US-10-257-017B-360215	Sequence 3
c 220	9.8	75.4	49.0	13	51	US-10-708-952A-102785	Sequence 1	c 293	9.75	45.0	45.0	12	40	US-10-257-017B-365894	Sequence 3
c 221	9.8	75.4	49.0	13	51	US-10-708-952A-105521	Sequence 1	c 294	9.75	45.0	45.0	12	40	US-10-257-017B-369635	Sequence 3
c 222	9.8	75.4	49.0	13	51	US-10-708-952A-281446	Sequence 2	c 295	9.75	45.0	45.0	12	40	US-10-257-017B-369635	Sequence 3
c 223	9.8	75.4	49.0	13	51	US-10-708-952A-283324	Sequence 2	c 296	9.75	45.0	45.0	12	40	US-10-257-017B-379943	Sequence 3
c 224	9.8	75.4	49.0	13	51	US-10-708-952B-102785	Sequence 1	c 297	9.75	45.0	45.0	12	52	US-10-708-953-1574359	Sequence 1
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c 226	9.8	75.4	49.0	13	51	US-10-708-952B-281446	Sequence 2	c 299	9.75	45.0	45.0	12	52	US-10-708-953-2023470	Sequence 2
c 227	9.8	75.4	49.0	13	51	US-10-708-952B-283324	Sequence 5	c 300	9.75	45.0	45.0	12	53	US-10-708-953A-1574359	Sequence 1
c 228	9.8	75.4	49.0	13	52	US-10-708-953-519962	Sequence 6	c 301	9.75	45.0	45.0	12	53	US-10-708-953A-1983714	Sequence 2
c 229	9.8	75.4	49.0	13	52	US-10-708-953-683001	Sequence 7	c 302	9.75	45.0	45.0	12	53	US-10-708-953A-2023470	Sequence 2
c 230	9.8	75.4	49.0	13	52	US-10-708-953-755878	Sequence 8	c 303	9.75	45.0	45.0	12	53	US-10-708-953A-2107113	Sequence 2
c 231	9.8	75.4	49.0	13	52	US-10-708-953									

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C 311	10.4	74.3	52.0	14	53	US-10-709-572-147851	Sequence 1	C 384	8.8	73.3	44.0	12	47	US-10-591-442-27	Sequence 2
C 312	10.4	74.3	52.0	13	40	US-10-799-238-14	Sequence 6	C 385	8.8	73.3	44.0	12	48	US-10-591-442-29	Sequence 2
C 313	9.6	73.8	48.0	13	40	US-10-257-017B-61663	Sequence 6	C 386	8.8	73.3	44.0	12	48	US-10-591-442-45	Sequence 1
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C 317	11.8	73.8	59.0	16	33	US-09-870-161-5807	Sequence 5	C 390	8.8	73.3	44.0	12	51	US-10-708-952B-289071	Sequence 2
C 318	11.8	73.8	59.0	16	40	US-10-227-565-533	Sequence 5	391	8.8	73.3	44.0	12	52	US-10-708-953-391440	Sequence 3
C 319	11.8	73.8	59.0	16	41	US-10-287-949B-5807	Sequence 5	392	8.8	73.3	44.0	12	52	US-10-708-953-426502	Sequence 4
C 320	11.8	73.8	59.0	16	41	US-10-287-949B-5807	Sequence 5	393	8.8	73.3	44.0	12	52	US-10-708-953-448734	Sequence 4
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C 322	11.8	73.8	59.0	16	46	US-10-367-832A-533	Sequence 5	C 395	8.8	73.3	44.0	12	52	US-10-708-953-467798	Sequence 4
C 323	11.8	73.8	59.0	16	53	US-10-709-572-191130	Sequence 1	C 396	8.8	73.3	44.0	12	52	US-10-708-953-524180	Sequence 5
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C 325	11.8	73.8	59.0	16	63	US-11-088-219-5807	Sequence 5	398	8.8	73.3	44.0	12	52	US-10-708-953-770756	Sequence 7
C 326	11.8	73.8	59.0	16	63	US-11-088-219A-5807	Sequence 5	399	8.8	73.3	44.0	12	52	US-10-708-953-787100	Sequence 7
C 327	14	73.7	70.0	19	2	PCT-US03-36787-764639	Sequence 7	C 400	8.8	73.3	44.0	12	52	US-10-708-953-863477	Sequence 8
C 328	14	73.7	70.0	19	54	US-10-714-333A-764639	Sequence 7	C 401	8.8	73.3	44.0	12	52	US-10-708-953-924430	Sequence 9
C 329	14	73.7	70.0	19	55	US-10-714-333B-764639	Sequence 7	C 402	8.8	73.3	44.0	12	52	US-10-708-953-925708	Sequence 9
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C 347	11	73.3	55.0	15	33	US-09-870-161-4150	Sequence 4	C 420	8.8	73.3	44.0	12	52	US-10-708-953-2206794	Sequence 2
C 348	11	73.3	55.0	15	41	US-10-287-949A-4150	Sequence 4	C 421	8.8	73.3	44.0	12	53	US-10-708-953A-391440	Sequence 3
C 349	11	73.3	55.0	15	41	US-10-287-949B-4150	Sequence 4	C 422	8.8	73.3	44.0	12	53	US-10-708-953A-426502	Sequence 4
C 350	11	73.3	55.0	15	41	US-10-287-949C-4150	Sequence 4	C 423	8.8	73.3	44.0	12	53	US-10-708-953A-448734	Sequence 4
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C 352	11	73.3	55.0	15	60	US-10-951-303B-4150	Sequence 4	C 425	8.8	73.3	44.0	12	53	US-10-708-953A-467798	Sequence 4
C 353	11	73.3	55.0	15	60	US-10-951-303B-4150	Sequence 4	C 426	8.8	73.3	44.0	12	53	US-10-708-953A-524180	Sequence 5
C 354	11	73.3	55.0	15	63	US-11-088-219-4150	Sequence 4	C 427	8.8	73.3	44.0	12	53	US-10-708-953A-524180	Sequence 5
C 355	11	73.3	55.0	12	1	PCT-IL05-00263-27	Sequence 2	C 428	8.8	73.3	44.0	12	53	US-10-708-953A-752554	Sequence 7
C 356	8.8	73.3	44.0	12	1	PCT-IL05-00263-29	Sequence 2	C 429	8.8	73.3	44.0	12	53	US-10-708-953A-770756	Sequence 7
C 357	8.8	73.3	44.0	12	1	PCT-IL05-00263-45	Sequence 2	C 430	8.8	73.3	44.0	12	53	US-10-708-953A-787100	Sequence 7
C 358	8.8	73.3	44.0	12	1	PCT-US02-15103A-15	Sequence 1	C 431	8.8	73.3	44.0	12	53	US-10-708-953A-863477	Sequence 8
C 359	8.8	73.3	44.0	12	3	PCT-US07-68401-1512	Sequence 1	C 432	8.8	73.3	44.0	12	53	US-10-708-953A-924430	Sequence 9
C 360	8.8	73.3	44.0	12	3	PCT-US07-68402-1512	Sequence 1	C 433	8.8	73.3	44.0	12	53	US-10-708-953A-925708	Sequence 9
C 361	8.8	73.3	44.0	12	3	PCT-US07-68403-1512	Sequence 1	C 434	8.8	73.3	44.0	12	53	US-10-708-953A-958234	Sequence 9
C 362	8.8	73.3	44.0	12	3	PCT-US07-68404-1512	Sequence 1	C 435	8.8	73.3	44.0	12	53	US-10-708-953A-1033680	Sequence 1
C 363	8.8	73.3	44.0	12	3	PCT-US07-68406-1512	Sequence 1	C 436	8.8	73.3	44.0	12	53	US-10-708-953A-1041658	Sequence 1
C 364	8.8	73.3	44.0	12	3	PCT-US07-68408-1512	Sequence 1	C 437	8.8	73.3	44.0	12	53	US-10-708-953A-1342582	Sequence 1
C 365	8.8	73.3	44.0	12	3	PCT-US07-68410-1512	Sequence 1	C 438	8.8	73.3	44.0	12	53	US-10-708-953A-1378924	Sequence 1
C 366	8.8	73.3	44.0	12	3	PCT-US07-68412-1512	Sequence 1	C 439	8.8	73.3	44.0	12	53	US-10-708-953A-1380444	Sequence 1
C 367	8.8	73.3	44.0	12	21	US-09-523-552-33	Sequence 2	C 440	8.8	73.3	44.0	12	53	US-10-708-953A-1539333	Sequence 1
C 368	8.8	73.3	44.0	12	21	US-09-523-552-22	Sequence 2	C 441	8.8	73.3	44.0	12	53	US-10-708-953A-1669231	Sequence 1
C 369	8.8	73.3	44.0	12	24	US-10-004-382-22	Sequence 2	C 442	8.8	73.3	44.0	12	53	US-10-708-953A-1754748	Sequence 1
C 370	8.8	73.3	44.0	12	38	US-10-257-017B-275104	Sequence 2	C 443	8.8	73.3	44.0	12	53	US-10-708-953A-1858055	Sequence 1
C 371	8.8	73.3	44.0	12	40	US-10-257-017B-290891	Sequence 2	C 444	8.8	73.3	44.0	12	53	US-10-708-953A-1868045	Sequence 1
C 372	8.8	73.3	44.0	12	40	US-10-257-017B-317181	Sequence 2	C 445	8.8	73.3	44.0	12	53	US-10-708-953A-1868720	Sequence 1
C 373	8.8	73.3	44.0	12	40	US-10-257-017B-322885	Sequence 3	C 446	8.8	73.3	44.0	12	53	US-10-708-953A-2003791	Sequence 2
C 374	8.8	73.3	44.0	12	40	US-10-257-017B-326883	Sequence 3	C 447	8.8	73.3	44.0	12	53	US-10-708-953A-2054387	Sequence 2
C 375	8.8	73.3	44.0	12	40	US-10-257-017B-326883	Sequence 3	C 448	8.8	73.3	44.0	12	53	US-10-708-953A-2142733	Sequence 2
C 376	8.8	73.3	44.0	12	40	US-10-257-017B-326883	Sequence 3	C 449	8.8	73.3	44.0	12	53		
C 377	8.8	73.3	44.0	12	40	US-10-257-017B-327149	Sequence 3	C 450	8.8	73.3	44.0	12	53		

C 451	8.8	73.3	44.0	12	53	US-10-708-953A-2179457	Sequence 2	524	9.4	72.3	47.0	13	51	US-10-708-952B-364482	Sequence 3
C 452	8.8	73.3	44.0	12	53	US-10-708-953A-2206794	Sequence 2	525	9.4	72.3	47.0	13	52	US-10-708-953-407469	Sequence 4
C 453	8.8	73.3	44.0	12	53	US-10-708-572-190034	Sequence 1	C 526	9.4	72.3	47.0	13	52	US-10-708-953-447891	Sequence 4
C 454	8.8	73.3	44.0	12	53	US-10-708-572-225526	Sequence 2	C 527	9.4	72.3	47.0	13	52	US-10-708-953-470264	Sequence 4
C 455	8.8	73.3	44.0	12	53	US-10-708-572-258617	Sequence 2	C 528	9.4	72.3	47.0	13	52	US-10-708-953-472685	Sequence 4
C 456	8.8	73.3	44.0	12	53	US-10-708-572-260004	Sequence 1	C 529	9.4	72.3	47.0	13	52	US-10-708-953-524505	Sequence 5
C 457	8.8	73.3	44.0	12	66	US-11-126-421-15	Sequence 2	C 530	9.4	72.3	47.0	13	52	US-10-708-953-578960	Sequence 5
C 458	8.8	73.3	44.0	12	75	US-11-438-135-357	Sequence 3	C 531	9.4	72.3	47.0	13	52	US-10-708-953-753472	Sequence 7
C 459	8.8	73.3	44.0	12	75	US-11-438-135-358	Sequence 3	C 532	9.4	72.3	47.0	13	52	US-10-708-953-804253	Sequence 8
C 460	8.8	73.3	44.0	12	78	US-11-588-939A-7	Sequence 7	C 533	9.4	72.3	47.0	13	52	US-10-708-953-869690	Sequence 8
C 461	8.8	73.3	44.0	12	81	US-11-745-429-1512	Sequence 1	C 534	9.4	72.3	47.0	13	52	US-10-708-953-956183	Sequence 9
C 462	8.8	73.3	44.0	12	81	US-11-799-117-48	Sequence 4	C 535	9.4	72.3	47.0	13	52	US-10-708-953-1053507	Sequence 9
C 463	8.8	73.3	44.0	12	87	US-60-244-692-22	Sequence 2	C 536	9.4	72.3	47.0	13	52	US-10-708-953-1090140	Sequence 1
C 464	12.4	72.9	62.0	17	25	US-09-546-745A-4860	Sequence 4	C 537	9.4	72.3	47.0	13	52	US-10-708-953-1150335	Sequence 1
C 465	12.4	72.9	62.0	17	25	US-09-546-745A-4861	Sequence 4	C 538	9.4	72.3	47.0	13	52	US-10-708-953-1181122	Sequence 1
C 466	12.4	72.9	62.0	17	49	US-10-603-923-508977	Sequence 5	C 539	9.4	72.3	47.0	13	52	US-10-708-953-1188461	Sequence 1
C 467	16	72.7	80.0	22	3	PCT-US05-37925-39	Sequence 3	C 540	9.4	72.3	47.0	13	52	US-10-708-953-1199339	Sequence 1
C 468	16	72.7	80.0	22	3	PCT-US05-37925-51	Sequence 5	C 541	9.4	72.3	47.0	13	52	US-10-708-953-1341689	Sequence 1
C 469	16	72.7	80.0	22	3	PCT-US06-00086-6	Sequence 6	C 542	9.4	72.3	47.0	13	52	US-10-708-953-1437920	Sequence 1
C 470	13.8	72.6	69.0	19	49	US-10-605-923-810848	Sequence 8	C 543	9.4	72.3	47.0	13	52	US-10-708-953-1484405	Sequence 1
C 471	13.8	72.6	69.0	19	50	US-10-605-924-801404	Sequence 8	C 544	9.4	72.3	47.0	13	52	US-10-708-953-1508698	Sequence 1
C 472	9.4	72.3	47.0	13	24	US-09-528-209A-6207	Sequence 6	C 545	9.4	72.3	47.0	13	52	US-10-708-953-1540033	Sequence 1
C 473	9.4	72.3	47.0	13	40	US-10-257-017B-6223	Sequence 6	C 546	9.4	72.3	47.0	13	52	US-10-708-953-1642533	Sequence 1
C 474	9.4	72.3	47.0	13	40	US-10-257-017B-6224	Sequence 6	C 547	9.4	72.3	47.0	13	52	US-10-708-953-1648335	Sequence 1
C 475	9.4	72.3	47.0	13	40	US-10-257-017B-12629	Sequence 1	C 548	9.4	72.3	47.0	13	52	US-10-708-953-1676486	Sequence 1
C 476	9.4	72.3	47.0	13	40	US-10-257-017B-12629	Sequence 1	C 549	9.4	72.3	47.0	13	52	US-10-708-953-1731944	Sequence 1
C 477	9.4	72.3	47.0	13	40	US-10-257-017B-25055	Sequence 2	C 550	9.4	72.3	47.0	13	52	US-10-708-953-174724	Sequence 1
C 478	9.4	72.3	47.0	13	40	US-10-257-017B-25055	Sequence 2	C 551	9.4	72.3	47.0	13	52	US-10-708-953-1747813	Sequence 1
C 479	9.4	72.3	47.0	13	40	US-10-257-017B-25056	Sequence 2	C 552	9.4	72.3	47.0	13	52	US-10-708-953-1765468	Sequence 1
C 480	9.4	72.3	47.0	13	40	US-10-257-017B-25081	Sequence 2	C 553	9.4	72.3	47.0	13	52	US-10-708-953-1847452	Sequence 1
C 481	9.4	72.3	47.0	13	40	US-10-257-017B-25082	Sequence 2	C 554	9.4	72.3	47.0	13	52	US-10-708-953-1859282	Sequence 1
C 482	9.4	72.3	47.0	13	40	US-10-257-017B-27969	Sequence 2	C 555	9.4	72.3	47.0	13	52	US-10-708-953-1859357	Sequence 1
C 483	9.4	72.3	47.0	13	40	US-10-257-017B-27970	Sequence 2	C 556	9.4	72.3	47.0	13	52	US-10-708-953-1981793	Sequence 1
C 484	9.4	72.3	47.0	13	40	US-10-257-017B-36537	Sequence 3	C 557	9.4	72.3	47.0	13	52	US-10-708-953-1988331	Sequence 1
C 485	9.4	72.3	47.0	13	40	US-10-257-017B-36538	Sequence 3	C 558	9.4	72.3	47.0	13	52	US-10-708-953-2045464	Sequence 2
C 486	9.4	72.3	47.0	13	40	US-10-257-017B-56753	Sequence 5	C 559	9.4	72.3	47.0	13	52	US-10-708-953-2074065	Sequence 2
C 487	9.4	72.3	47.0	13	40	US-10-257-017B-56754	Sequence 5	C 560	9.4	72.3	47.0	13	52	US-10-708-953-2105665	Sequence 2
C 488	9.4	72.3	47.0	13	40	US-10-257-017B-96865	Sequence 9	C 561	9.4	72.3	47.0	13	52	US-10-708-953-2145797	Sequence 2
C 489	9.4	72.3	47.0	13	40	US-10-257-017B-96866	Sequence 9	C 562	9.4	72.3	47.0	13	52	US-10-708-953-2156391	Sequence 2
C 490	9.4	72.3	47.0	13	40	US-10-257-017B-111321	Sequence 1	C 563	9.4	72.3	47.0	13	52	US-10-708-953-2195838	Sequence 2
C 491	9.4	72.3	47.0	13	40	US-10-257-017B-111322	Sequence 1	C 564	9.4	72.3	47.0	13	52	US-10-708-953-2219670	Sequence 2
C 492	9.4	72.3	47.0	13	40	US-10-257-017B-117287	Sequence 1	C 565	9.4	72.3	47.0	13	53	US-10-708-953A-407469	Sequence 4
C 493	9.4	72.3	47.0	13	40	US-10-257-017B-117288	Sequence 1	C 566	9.4	72.3	47.0	13	53	US-10-708-953A-447891	Sequence 4
C 494	9.4	72.3	47.0	13	40	US-10-257-017B-117509	Sequence 1	C 567	9.4	72.3	47.0	13	53	US-10-708-953A-470264	Sequence 4
C 495	9.4	72.3	47.0	13	40	US-10-257-017B-117510	Sequence 1	C 568	9.4	72.3	47.0	13	53	US-10-708-953A-472685	Sequence 4
C 496	9.4	72.3	47.0	13	40	US-10-257-017B-187027	Sequence 1	C 569	9.4	72.3	47.0	13	53	US-10-708-953A-524505	Sequence 5
C 497	9.4	72.3	47.0	13	40	US-10-257-017B-187028	Sequence 1	C 570	9.4	72.3	47.0	13	53	US-10-708-953A-578960	Sequence 5
C 498	9.4	72.3	47.0	13	40	US-10-257-017B-215785	Sequence 2	C 571	9.4	72.3	47.0	13	53	US-10-708-953A-753472	Sequence 7
C 499	9.4	72.3	47.0	13	40	US-10-257-017B-215786	Sequence 2	C 572	9.4	72.3	47.0	13	53	US-10-708-953A-804253	Sequence 8
C 500	9.4	72.3	47.0	13	40	US-10-257-017B-235787	Sequence 2	C 573	9.4	72.3	47.0	13	53	US-10-708-953A-869690	Sequence 8
C 501	9.4	72.3	47.0	13	40	US-10-257-017B-235788	Sequence 2	C 574	9.4	72.3	47.0	13	53	US-10-708-953A-956183	Sequence 9
C 502	9.4	72.3	47.0	13	40	US-10-257-017B-248349	Sequence 2	C 575	9.4	72.3	47.0	13	53	US-10-708-953A-1053507	Sequence 1
C 503	9.4	72.3	47.0	13	40	US-10-257-017B-248350	Sequence 2	C 576	9.4	72.3	47.0	13	53	US-10-708-953A-1090140	Sequence 1
C 504	9.4	72.3	47.0	13	51	US-10-708-952A-214716	Sequence 2	C 577	9.4	72.3	47.0	13	53	US-10-708-953A-1150335	Sequence 1
C 505	9.4	72.3	47.0	13	51	US-10-708-952A-215927	Sequence 2	C 578	9.4	72.3	47.0	13	53	US-10-708-953A-1181122	Sequence 1
C 506	9.4	72.3	47.0	13	51	US-10-708-952A-217681	Sequence 2	C 579	9.4	72.3	47.0	13	53	US-10-708-953A-1188461	Sequence 1
C 507	9.4	72.3	47.0	13	51	US-10-708-952A-217760	Sequence 2	C 580	9.4	72.3	47.0	13	53	US-10-708-953A-1199339	Sequence 1
C 508	9.4	72.3	47.0	13	51	US-10-708-952A-219831	Sequence 2	C 581	9.4	72.3	47.0	13	53	US-10-708-953A-1341689	Sequence 1
C 509	9.4	72.3	47.0	13	51	US-10-708-952A-221139	Sequence 2	C 582	9.4	72.3	47.0	13	53	US-10-708-953A-1437920	Sequence 1
C 510	9.4	72.3	47.0	13	51	US-10-708-952A-226704	Sequence 2	C 583	9.4	72.3	47.0	13	53	US-10-708-953A-1484405	Sequence 1
C 511	9.4	72.3	47.0	13	51	US-10-708-952A-25681	Sequence 2	C 584	9.4	72.3	47.0	13	53	US-10-708-953A-1508698	Sequence 1
C 512	9.4	72.3	47.0	13	51	US-10-708-952A-260591	Sequence 2	C 585	9.4	72.3	47.0	13	53	US-10-708-953A-1540033	Sequence 1
C 513	9.4	72.3	47.0	13	51	US-10-708-952A-272157	Sequence 3	C 586	9.4	72.3	47.0	13	53	US-10-708-953A-1642533	Sequence 1
C 514	9.4	72.3	47.0	13	51	US-10-708-952A-364482	Sequence 2	C 587	9.4	72.3	47.0	13	53	US-10-708-953A-1648335	Sequence 1
C 515	9.4	72.3	47.0	13	51	US-10-708-952B-214716	Sequence 2	C 588	9.4	72.3	47.0	13	53	US-10-708-953A-1731944	Sequence 1
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C 521	9.4	72.3	47.0	13	51	US-10-708-952B-226704	Sequence 2	C 594	9.4	72.3	47.0	13	53	US-10-708-953A-1859282	Sequence 1
C 522	9.4	72.3	47.0	13	51	US-10-708-952B-252681	Sequence 2	C 595	9.4	72.3	47.0	13	53	US-10-708-953A-1969357	Sequence 1
C 523	9.4	72.3	47.0	13	51	US-10-708-952B-260591	Sequence 2	C 596	9.4	72.3	47.0	13	53	US-10-708-953A-1981793	Sequence 1

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c 598	9.4	72.3	47.0	13	53	US-10-708-953A-2045464	Sequence 2	C 671	10	71.4	50.0	14	52	US-10-708-953-1803862	Sequence 2
599	9.4	72.3	47.0	13	53	US-10-708-953A-2074065	Sequence 2	C 672	10	71.4	50.0	14	52	US-10-708-953-2215675	Sequence 5
c 600	9.4	72.3	47.0	13	53	US-10-708-953A-2105665	Sequence 2	C 673	10	71.4	50.0	14	53	US-10-708-953A-559363	Sequence 8
c 601	9.4	72.3	47.0	13	53	US-10-708-953A-2145797	Sequence 2	C 674	10	71.4	50.0	14	53	US-10-708-953A-809991	Sequence 1
c 602	9.4	72.3	47.0	13	53	US-10-708-953A-2156391	Sequence 2	C 675	10	71.4	50.0	14	53	US-10-708-953A-1161164	Sequence 1
c 603	9.4	72.3	47.0	13	53	US-10-708-953A-2195838	Sequence 2	C 676	10	71.4	50.0	14	53	US-10-708-953A-1580045	Sequence 1
c 604	9.4	72.3	47.0	13	53	US-10-708-953A-2219670	Sequence 2	C 677	10	71.4	50.0	14	53	US-10-708-953A-1803862	Sequence 1
c 605	9.4	72.3	47.0	13	53	US-10-708-953A-2253375	Sequence 1	C 678	10	71.4	50.0	14	53	US-10-708-953A-2215675	Sequence 2
c 606	9.4	72.3	47.0	13	53	US-10-708-953A-2253375	Sequence 1	C 679	10	71.4	50.0	14	60	US-10-708-953A-2215675	Sequence 2
c 607	9.4	72.3	47.0	13	53	US-10-708-953A-2253375	Sequence 1	C 680	10	71.4	50.0	14	81	US-11-745-423-329	Sequence 3
c 608	9.4	72.3	47.0	13	53	US-10-708-953A-2253375	Sequence 1	C 681	11.4	71.2	57.0	16	41	US-10-287-813-559	Sequence 5
c 609	9.4	72.3	47.0	13	53	US-10-708-953A-2253375	Sequence 1	C 682	12.8	71.1	64.0	18	50	US-10-605-924-1258144	Sequence 1
c 610	10.8	72.0	54.0	15	1	PCT-US02-25940-144	Sequence 1	C 683	12.8	71.1	64.0	18	53	US-10-708-953A-1803862	Sequence 2
c 611	10.8	72.0	54.0	15	1	PCT-US02-25940-144	Sequence 2	C 684	12.8	71.1	64.0	18	62	US-11-045-005-541	Sequence 5
c 612	10.8	72.0	54.0	15	1	PCT-US02-25940-144	Sequence 3	C 685	12.8	71.1	64.0	18	63	US-11-084-847-541	Sequence 9
c 613	10.8	72.0	54.0	15	1	PCT-US02-25940-144	Sequence 4	C 686	17	70.8	85.0	24	3	PCT-US06-00086-9	Sequence 1
c 614	10.8	72.0	54.0	15	40	US-10-227-563-282	Sequence 1	C 687	17	70.8	85.0	24	3	PCT-US06-00086-9	Sequence 2
c 615	10.8	72.0	54.0	15	40	US-10-227-563-282	Sequence 2	C 688	10.6	70.7	53.0	15	1	PCT-US01-47394-27	Sequence 1
c 616	10.8	72.0	54.0	15	40	US-10-227-564-4166	Sequence 4	C 689	10.6	70.7	53.0	15	39	US-10-160-358-26	Sequence 2
c 617	10.8	72.0	54.0	15	40	US-10-227-564-4166	Sequence 4	C 690	12	70.6	60.0	17	1	PCT-US02-17674-3654	Sequence 3
c 618	10.8	72.0	54.0	15	41	US-10-299-054A-4598	Sequence 1	C 691	12	70.6	60.0	17	30	US-09-708-690-1647	Sequence 1
c 619	10.8	72.0	54.0	15	46	US-10-321-854-2304	Sequence 2	C 692	12	70.6	60.0	17	30	US-09-708-690-1647	Sequence 6
c 620	10.8	72.0	54.0	15	46	US-10-364-412A-4166	Sequence 4	C 693	12	70.6	60.0	17	30	US-09-708-690-1647	Sequence 6
c 621	10.8	72.0	54.0	15	46	US-10-364-412A-4166	Sequence 4	C 694	12	70.6	60.0	17	30	US-09-708-690-1647	Sequence 8
c 622	10.8	72.0	54.0	15	46	US-10-367-892-144	Sequence 1	C 695	12	70.6	60.0	17	33	US-09-870-161-1647	Sequence 1
c 623	10.8	72.0	54.0	15	46	US-10-367-892-144	Sequence 2	C 696	12	70.6	60.0	17	33	US-09-870-161-1647	Sequence 1
c 624	10.8	72.0	54.0	15	49	US-10-604-985-8387	Sequence 8	C 697	12	70.6	60.0	17	33	US-09-870-161-1647	Sequence 6
c 625	10.8	72.0	54.0	15	49	US-10-604-985-8387	Sequence 8	C 698	12	70.6	60.0	17	33	US-09-870-161-1647	Sequence 6
c 626	10.8	72.0	54.0	15	51	US-10-708-952A-104569	Sequence 1	C 699	12	70.6	60.0	17	33	US-09-870-161-1647	Sequence 8
c 627	10.8	72.0	54.0	15	51	US-10-708-952A-104569	Sequence 1	C 700	12	70.6	60.0	17	41	US-10-287-949A-1647	Sequence 1
c 628	10.8	72.0	54.0	15	51	US-10-708-952A-105423	Sequence 2	C 701	12	70.6	60.0	17	41	US-10-287-949A-1647	Sequence 1
c 629	10.8	72.0	54.0	15	51	US-10-708-952A-105423	Sequence 2	C 702	12	70.6	60.0	17	41	US-10-287-949A-1647	Sequence 6
c 630	10.8	72.0	54.0	15	51	US-10-708-952A-105423	Sequence 2	C 703	12	70.6	60.0	17	41	US-10-287-949A-1647	Sequence 6
c 631	10.8	72.0	54.0	15	51	US-10-708-952A-105423	Sequence 2	C 704	12	70.6	60.0	17	41	US-10-287-949A-1647	Sequence 6
c 632	10.8	72.0	54.0	15	51	US-10-708-952B-104569	Sequence 1	C 705	12	70.6	60.0	17	41	US-10-287-949B-1647	Sequence 1
c 633	10.8	72.0	54.0	15	51	US-10-708-952B-104569	Sequence 2	C 706	12	70.6	60.0	17	41	US-10-287-949B-1647	Sequence 6
c 634	10.8	72.0	54.0	15	51	US-10-708-952B-104569	Sequence 2	C 707	12	70.6	60.0	17	41	US-10-287-949B-1647	Sequence 6
c 635	10.8	72.0	54.0	15	52	US-10-708-953-545642	Sequence 5	C 708	12	70.6	60.0	17	41	US-10-287-949B-1647	Sequence 6
c 636	10.8	72.0	54.0	15	52	US-10-708-953-1724380	Sequence 1	C 709	12	70.6	60.0	17	41	US-10-287-949B-1647	Sequence 8
c 637	10.8	72.0	54.0	15	52	US-10-708-953-2042003	Sequence 2	C 710	12	70.6	60.0	17	41	US-10-287-949C-1646	Sequence 1
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c 639	10.8	72.0	54.0	15	53	US-10-708-953A-1724380	Sequence 1	C 712	12	70.6	60.0	17	41	US-10-287-949C-1647	Sequence 6
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c 644	10.8	72.0	54.0	15	53	US-10-708-953A-2053033	Sequence 1	C 717	12	70.6	60.0	17	60	US-10-951-303-1647	Sequence 1
c 645	10.8	72.0	54.0	15	58	US-10-834-967-1289	Sequence 1	C 718	12	70.6	60.0	17	60	US-10-951-303-1647	Sequence 1
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c 647	12.2	71.8	61.0	17	41	US-10-299-054A-2636	Sequence 2	C 720	12	70.6	60.0	17	60	US-10-951-303B-1647	Sequence 1
c 648	12.2	71.8	61.0	17	41	US-10-299-054A-2636	Sequence 2	C 721	12	70.6	60.0	17	63	US-11-088-219-1647	Sequence 1
c 649	10	71.4	50.0	14	3	PCT-US07-68401-329	Sequence 3	C 722	12	70.6	60.0	17	63	US-11-088-219-1647	Sequence 6
c 650	10	71.4	50.0	14	3	PCT-US07-68401-329	Sequence 3	C 723	12	70.6	60.0	17	63	US-11-088-219-1647	Sequence 6
c 651	10	71.4	50.0	14	3	PCT-US07-68401-329	Sequence 3	C 724	12	70.6	60.0	17	63	US-11-088-219-1647	Sequence 8
c 652	10	71.4	50.0	14	3	PCT-US07-68401-329	Sequence 3	C 725	12	70.6	60.0	17	63	US-11-088-219-1647	Sequence 8
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c 655	10	71.4	50.0	14	3	PCT-US07-68401-329	Sequence 3	C 728	12	70.6	60.0	17	63	US-11-088-219A-1647	Sequence 6
c 656	10	71.4	50.0	14	3	PCT-US07-68401-329	Sequence 3	C 729	12	70.6	60.0	17	63	US-11-088-219A-1647	Sequence 8
c 657	10	71.4	50.0	14	14	US-08-591-486B-34	Sequence 3	C 730	12	70.6	60.0	17	63	US-11-088-219A-1647	Sequence 8
c 658	10	71.4	50.0	14	14	US-08-591-486B-34	Sequence 3	C 731	12	70.6	60.0	17	76	US-11-475-062-8179	Sequence 7
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c 660	10	71.4	50.0	14	51	US-10-708-952A-180197	Sequence 1	C 733	13.4	70.5	67.0	19	2	PCT-US03-36787-726378	Sequence 7
c 661	10	71.4	50.0	14	51	US-10-708-952A-180197	Sequence 1	C 734	13.4	70.5	67.0	19	2	PCT-US03-36787-1192689	Sequence 1
c 662	10	71.4	50.0	14	51	US-10-708-952A-348556	Sequence 1	C 735	13.4	70.5	67.0	19	2	PCT-US03-36787-1192689	Sequence 1
c 663	10	71.4	50.0	14	51	US-10-708-952A-348556	Sequence 1	C 736	13.4	70.5	67.0	19	2	PCT-US03-36787-1192689	Sequence 1
c 664	10	71.4	50.0	14	51	US-10-708-952B-178861	Sequence 1	C 737	13.4	70.5	67.0	19	50	US-10-605-924-1191074	Sequence 1
c 665	10	71.4	50.0	14	51	US-10-708-952B-180197	Sequence 1	C 738	13.4	70.5	67.0	19	54	US-10-714-333A-726378	Sequence 7
c 666	10	71.4	50.0	14	51	US-10-708-952B-180197	Sequence 1	C 739	13.4	70.5	67.0	19	54	US-10-714-333A-726378	Sequence 7
c 667	10	71.4	50.0	14	52	US-10-708-953-559363	Sequence 5	C 740	13.4	70.5	67.0	19	54	US-10-714-333A-1192689	Sequence 1
c 668	10	71.4	50.0	14	52	US-10-708-953-559363	Sequence 5	C 741	13.4	70.5	67.0	19	54	US-10-714-333A-1192689	Sequence 1
c 669	10	71.4	50.0	14	52	US-10-708-953-1161164	Sequence 1	C 742	13.4	70.5	67.0	19	54	US-10-714-333A-1192689	Sequence 1

C 743	13.4	70.5	67.0	19	55	US-10-714-333B-726378	Sequence 7	C 816	9.8	70.0	49.0	14	52	US-10-708-953-756503	Sequence 7
C 744	13.4	70.5	67.0	19	55	US-10-714-333B-726385	Sequence 7	C 817	9.8	70.0	49.0	14	52	US-10-708-953-787966	Sequence 7
C 745	13.4	70.5	67.0	19	55	US-10-714-333B-1192689	Sequence 1	818	9.8	70.0	49.0	14	52	US-10-708-953-801220	Sequence 8
C 746	13.4	70.5	67.0	19	55	US-10-714-333B-1192696	Sequence 1	819	9.8	70.0	49.0	14	52	US-10-708-953-858746	Sequence 8
C 747	13.4	70.5	67.0	19	55	US-10-714-333B-1192704	Sequence 1	820	9.8	70.0	49.0	14	52	US-10-708-953-930627	Sequence 9
C 748	13.4	70.5	67.0	19	56	US-10-714-333C-726378	Sequence 7	C 821	9.8	70.0	49.0	14	52	US-10-708-953-1000343	Sequence 1
C 749	13.4	70.5	67.0	19	56	US-10-714-333C-726385	Sequence 7	C 822	9.8	70.0	49.0	14	52	US-10-708-953-1132564	Sequence 1
C 750	13.4	70.5	67.0	19	56	US-10-714-333C-1192689	Sequence 1	C 823	9.8	70.0	49.0	14	52	US-10-708-953-1188181	Sequence 1
C 751	13.4	70.5	67.0	19	56	US-10-714-333C-1192696	Sequence 1	C 824	9.8	70.0	49.0	14	52	US-10-708-953-1250851	Sequence 1
C 752	13.4	70.5	67.0	19	56	US-10-714-333C-1192704	Sequence 1	C 825	9.8	70.0	49.0	14	52	US-10-708-953-1317930	Sequence 1
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C 754	13.4	70.5	67.0	19	63	US-11-083-784-726385	Sequence 7	C 827	9.8	70.0	49.0	14	52	US-10-708-953-1372275	Sequence 1
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C 757	13.4	70.5	67.0	19	63	US-11-083-784-1192704	Sequence 1	C 830	9.8	70.0	49.0	14	52	US-10-708-953-1625566	Sequence 1
C 758	13.4	70.5	67.0	19	64	US-11-093-832-726378	Sequence 7	C 831	9.8	70.0	49.0	14	52	US-10-708-953-1777980	Sequence 1
C 759	13.4	70.5	67.0	19	64	US-11-093-832-726385	Sequence 7	C 832	9.8	70.0	49.0	14	52	US-10-708-953-1813012	Sequence 1
C 760	13.4	70.5	67.0	19	64	US-11-093-832-1192689	Sequence 1	C 833	9.8	70.0	49.0	14	52	US-10-708-953-1815082	Sequence 1
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C 763	13.4	70.5	67.0	19	65	US-11-095-383-726378	Sequence 7	C 836	9.8	70.0	49.0	14	52	US-10-708-953-1857410	Sequence 1
C 764	13.4	70.5	67.0	19	65	US-11-095-383-726385	Sequence 7	C 837	9.8	70.0	49.0	14	52	US-10-708-953-1971834	Sequence 1
C 765	13.4	70.5	67.0	19	65	US-11-095-383-1192689	Sequence 1	C 838	9.8	70.0	49.0	14	52	US-10-708-953-2125666	Sequence 2
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C 768	13.4	70.5	67.0	19	66	US-11-101-244-726378	Sequence 7	C 841	9.8	70.0	49.0	14	53	US-10-708-953A-418459	Sequence 4
C 769	13.4	70.5	67.0	19	66	US-11-101-244-726385	Sequence 7	C 842	9.8	70.0	49.0	14	53	US-10-708-953A-438494	Sequence 4
C 770	13.4	70.5	67.0	19	66	US-11-101-244-1192689	Sequence 1	C 843	9.8	70.0	49.0	14	53	US-10-708-953A-549103	Sequence 5
C 771	13.4	70.5	67.0	19	66	US-11-101-244-1192696	Sequence 1	C 844	9.8	70.0	49.0	14	53	US-10-708-953A-591354	Sequence 5
C 772	13.4	70.5	67.0	19	66	US-11-101-244-1192704	Sequence 1	C 845	9.8	70.0	49.0	14	53	US-10-708-953A-610006	Sequence 6
C 773	13.4	70.5	67.0	19	71	US-11-313-452-726378	Sequence 7	C 846	9.8	70.0	49.0	14	53	US-10-708-953A-631771	Sequence 6
C 774	13.4	70.5	67.0	19	71	US-11-313-452-726385	Sequence 7	C 847	9.8	70.0	49.0	14	53	US-10-708-953A-756503	Sequence 7
C 775	13.4	70.5	67.0	19	71	US-11-313-452-1192689	Sequence 1	C 848	9.8	70.0	49.0	14	53	US-10-708-953A-787966	Sequence 7
C 776	13.4	70.5	67.0	19	71	US-11-313-452-1192696	Sequence 1	C 849	9.8	70.0	49.0	14	53	US-10-708-953A-801220	Sequence 8
C 777	13.4	70.5	67.0	19	71	US-11-313-452-1192704	Sequence 1	C 850	9.8	70.0	49.0	14	53	US-10-708-953A-858746	Sequence 8
C 778	13.4	70.5	67.0	19	72	US-11-313-452A-726378	Sequence 7	C 851	9.8	70.0	49.0	14	53	US-10-708-953A-930627	Sequence 9
C 779	13.4	70.5	67.0	19	72	US-11-313-452A-726385	Sequence 7	C 852	9.8	70.0	49.0	14	53	US-10-708-953A-1000343	Sequence 9
C 780	13.4	70.5	67.0	19	72	US-11-313-452A-1192689	Sequence 1	C 853	9.8	70.0	49.0	14	53	US-10-708-953A-1132564	Sequence 1
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C 782	13.4	70.5	67.0	19	72	US-11-313-452A-1192704	Sequence 1	C 855	9.8	70.0	49.0	14	53	US-10-708-953A-1250851	Sequence 1
C 783	11.2	70.0	56.0	16	1	PCT-US02-25943-20371	Sequence 2	C 856	9.8	70.0	49.0	14	53	US-10-708-953A-1317930	Sequence 1
C 784	11.2	70.0	56.0	16	40	US-10-227-565-20371	Sequence 2	C 857	9.8	70.0	49.0	14	53	US-10-708-953A-1354289	Sequence 1
C 785	11.2	70.0	56.0	16	46	US-10-316-934-519	Sequence 5	C 858	9.8	70.0	49.0	14	53	US-10-708-953A-1372275	Sequence 1
C 786	11.2	70.0	56.0	16	46	US-10-367-832A-20371	Sequence 5	C 859	9.8	70.0	49.0	14	53	US-10-708-953A-1409428	Sequence 1
C 787	11.2	70.0	56.0	16	46	US-10-535-164-474753	Sequence 4	C 860	9.8	70.0	49.0	14	53	US-10-708-953A-1425356	Sequence 1
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C 792	9.8	70.0	49.0	14	51	US-10-708-952A-109561	Sequence 1	C 865	9.8	70.0	49.0	14	53	US-10-708-953A-1840939	Sequence 1
C 793	9.8	70.0	49.0	14	51	US-10-708-952A-109575	Sequence 1	C 866	9.8	70.0	49.0	14	53	US-10-708-953A-1857310	Sequence 1
C 794	9.8	70.0	49.0	14	51	US-10-708-952A-132354	Sequence 2	C 867	9.8	70.0	49.0	14	53	US-10-708-953A-1857410	Sequence 1
C 795	9.8	70.0	49.0	14	51	US-10-708-952A-282060	Sequence 2	C 868	9.8	70.0	49.0	14	53	US-10-708-953A-1971834	Sequence 1
C 796	9.8	70.0	49.0	14	51	US-10-708-952A-284069	Sequence 2	C 869	9.8	70.0	49.0	14	53	US-10-708-953A-2125666	Sequence 2
C 797	9.8	70.0	49.0	14	51	US-10-708-952A-288500	Sequence 2	C 870	9.8	70.0	49.0	14	53	US-10-708-953A-2198709	Sequence 2
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C 800	9.8	70.0	49.0	14	51	US-10-708-952B-102561	Sequence 1	C 873	9.8	70.0	49.0	14	53	US-10-709-572-157982	Sequence 1
C 801	9.8	70.0	49.0	14	51	US-10-708-952B-103254	Sequence 1	C 874	9.8	70.0	49.0	14	53	US-10-709-572-181309	Sequence 1
C 802	9.8	70.0	49.0	14	51	US-10-708-952B-109561	Sequence 1	C 875	9.8	70.0	49.0	14	53	US-10-709-572-194415	Sequence 1
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C 804	9.8	70.0	49.0	14	51	US-10-708-952B-132354	Sequence 1	C 877	9.8	70.0	49.0	14	53	US-10-709-572-202286	Sequence 2
C 805	9.8	70.0	49.0	14	51	US-10-708-952B-182060	Sequence 2	C 878	9.8	70.0	49.0	14	53	US-10-709-572-265453	Sequence 2
C 806	9.8	70.0	49.0	14	51	US-10-708-952B-284069	Sequence 2	C 879	9.8	70.0	49.0	14	53	US-10-709-572-294011	Sequence 2
C 807	9.8	70.0	49.0	14	51	US-10-708-952B-288500	Sequence 2	C 880	9.8	70.0	49.0	14	53	US-10-709-572-332589	Sequence 3
C 808	9.8	70.0	49.0	14	51	US-10-708-952B-303863	Sequence 3	C 881	9.8	70.0	49.0	12	3	PCT-US96-03186-16	Sequence 1
C 809	9.8	70.0	49.0	14	51	US-10-708-952B-304724	Sequence 3	C 882	8.4	70.0	42.0	12	3	PCT-US96-17132-48	Sequence 4
C 810	9.8	70.0	49.0	14	52	US-10-708-953-418459	Sequence 4	C 883	8.4	70.0	42.0	12	13	US-08-424-992-16	Sequence 1
C 811	9.8	70.0	49.0	14	52	US-10-708-953-438494	Sequence 4	C 884	8.4	70.0	42.0	12	16	US-08-784-200A-24	Sequence 2
C 812	9.8	70.0	49.0	14	52	US-10-708-953-549103	Sequence 5	C 885	8.4	70.0	42.0	12	17	US-08-883-128-16	Sequence 2
C 813	9.8	70.0	49.0	14	52	US-10-708-953-591354	Sequence 5	C 886	8.4	70.0	42.0	12	21	US-09-254-929-33	Sequence 3
C 814	9.8	70.0	49.0	14	52	US-10-708-953-610006	Sequence 6	C 887	8.4	70.0	42.0	12	36	US-09-983-446C-1730	Sequence 1
C 815	9.8	70.0	49.0	14	52	US-10-708-953-691771	Sequence 6	C 888	8.4	70.0	42.0	12	40	US-10-2	

C 889	8.4	70.0	42.0	12	40	US-10-257-017B-269582	Sequence 2
C 890	8.4	70.0	42.0	12	40	US-10-257-017B-269967	Sequence 2
C 891	8.4	70.0	42.0	12	40	US-10-257-017B-270364	Sequence 2
C 892	8.4	70.0	42.0	12	40	US-10-257-017B-270867	Sequence 2
C 893	8.4	70.0	42.0	12	40	US-10-257-017B-272438	Sequence 2
C 894	8.4	70.0	42.0	12	40	US-10-257-017B-272556	Sequence 2
C 895	8.4	70.0	42.0	12	40	US-10-257-017B-274200	Sequence 2
C 896	8.4	70.0	42.0	12	40	US-10-257-017B-274757	Sequence 2
C 897	8.4	70.0	42.0	12	40	US-10-257-017B-280041	Sequence 2
C 898	8.4	70.0	42.0	12	40	US-10-257-017B-281065	Sequence 2
C 899	8.4	70.0	42.0	12	40	US-10-257-017B-281930	Sequence 2
C 900	8.4	70.0	42.0	12	40	US-10-257-017B-284490	Sequence 2
C 901	8.4	70.0	42.0	12	40	US-10-257-017B-285659	Sequence 2
C 902	8.4	70.0	42.0	12	40	US-10-257-017B-286867	Sequence 2
C 903	8.4	70.0	42.0	12	40	US-10-257-017B-288407	Sequence 2
C 904	8.4	70.0	42.0	12	40	US-10-257-017B-290224	Sequence 2
C 905	8.4	70.0	42.0	12	40	US-10-257-017B-292658	Sequence 2
C 906	8.4	70.0	42.0	12	40	US-10-257-017B-292707	Sequence 2
C 907	8.4	70.0	42.0	12	40	US-10-257-017B-293121	Sequence 2
C 908	8.4	70.0	42.0	12	40	US-10-257-017B-293477	Sequence 2
C 909	8.4	70.0	42.0	12	40	US-10-257-017B-293667	Sequence 2
C 910	8.4	70.0	42.0	12	40	US-10-257-017B-294586	Sequence 2
C 911	8.4	70.0	42.0	12	40	US-10-257-017B-295090	Sequence 2
C 912	8.4	70.0	42.0	12	40	US-10-257-017B-295284	Sequence 2
C 913	8.4	70.0	42.0	12	40	US-10-257-017B-296295	Sequence 2
C 914	8.4	70.0	42.0	12	40	US-10-257-017B-296487	Sequence 2
C 915	8.4	70.0	42.0	12	40	US-10-257-017B-297323	Sequence 2
C 916	8.4	70.0	42.0	12	40	US-10-257-017B-298042	Sequence 2
C 917	8.4	70.0	42.0	12	40	US-10-257-017B-299239	Sequence 2
C 918	8.4	70.0	42.0	12	40	US-10-257-017B-299348	Sequence 2
C 919	8.4	70.0	42.0	12	40	US-10-257-017B-300438	Sequence 2
C 920	8.4	70.0	42.0	12	40	US-10-257-017B-302603	Sequence 2
C 921	8.4	70.0	42.0	12	40	US-10-257-017B-302958	Sequence 2
C 922	8.4	70.0	42.0	12	40	US-10-257-017B-304877	Sequence 2
C 923	8.4	70.0	42.0	12	40	US-10-257-017B-306204	Sequence 2
C 924	8.4	70.0	42.0	12	40	US-10-257-017B-306498	Sequence 2
C 925	8.4	70.0	42.0	12	40	US-10-257-017B-306928	Sequence 2
C 926	8.4	70.0	42.0	12	40	US-10-257-017B-309177	Sequence 2
C 927	8.4	70.0	42.0	12	40	US-10-257-017B-310209	Sequence 2
C 928	8.4	70.0	42.0	12	40	US-10-257-017B-310210	Sequence 2
C 929	8.4	70.0	42.0	12	40	US-10-257-017B-312793	Sequence 2
C 930	8.4	70.0	42.0	12	40	US-10-257-017B-316105	Sequence 2
C 931	8.4	70.0	42.0	12	40	US-10-257-017B-316407	Sequence 2
C 932	8.4	70.0	42.0	12	40	US-10-257-017B-316595	Sequence 2
C 933	8.4	70.0	42.0	12	40	US-10-257-017B-316596	Sequence 2
C 934	8.4	70.0	42.0	12	40	US-10-257-017B-317245	Sequence 2
C 935	8.4	70.0	42.0	12	40	US-10-257-017B-317868	Sequence 2
C 936	8.4	70.0	42.0	12	40	US-10-257-017B-317906	Sequence 2
C 937	8.4	70.0	42.0	12	40	US-10-257-017B-318475	Sequence 2
C 938	8.4	70.0	42.0	12	40	US-10-257-017B-321495	Sequence 2
C 939	8.4	70.0	42.0	12	40	US-10-257-017B-322078	Sequence 2
C 940	8.4	70.0	42.0	12	40	US-10-257-017B-323774	Sequence 2
C 941	8.4	70.0	42.0	12	40	US-10-257-017B-323855	Sequence 2
C 942	8.4	70.0	42.0	12	40	US-10-257-017B-327363	Sequence 2
C 943	8.4	70.0	42.0	12	40	US-10-257-017B-328966	Sequence 2
C 944	8.4	70.0	42.0	12	40	US-10-257-017B-329138	Sequence 2
C 945	8.4	70.0	42.0	12	40	US-10-257-017B-329589	Sequence 2
C 946	8.4	70.0	42.0	12	40	US-10-257-017B-329753	Sequence 2
C 947	8.4	70.0	42.0	12	40	US-10-257-017B-331303	Sequence 2
C 948	8.4	70.0	42.0	12	40	US-10-257-017B-331432	Sequence 2
C 949	8.4	70.0	42.0	12	40	US-10-257-017B-331579	Sequence 2
C 950	8.4	70.0	42.0	12	40	US-10-257-017B-331707	Sequence 2
C 951	8.4	70.0	42.0	12	40	US-10-257-017B-332215	Sequence 2
C 952	8.4	70.0	42.0	12	40	US-10-257-017B-333855	Sequence 2
C 953	8.4	70.0	42.0	12	40	US-10-257-017B-333880	Sequence 2
C 954	8.4	70.0	42.0	12	40	US-10-257-017B-336184	Sequence 2
C 955	8.4	70.0	42.0	12	40	US-10-257-017B-338774	Sequence 2
C 956	8.4	70.0	42.0	12	40	US-10-257-017B-338942	Sequence 2
C 957	8.4	70.0	42.0	12	40	US-10-257-017B-339290	Sequence 2
C 958	8.4	70.0	42.0	12	40	US-10-257-017B-341683	Sequence 2
C 959	8.4	70.0	42.0	12	40	US-10-257-017B-341694	Sequence 2
C 960	8.4	70.0	42.0	12	40	US-10-257-017B-341790	Sequence 2
C 961	8.4	70.0	42.0	12	40	US-10-257-017B-342185	Sequence 2
C 962	8.4	70.0	42.0	12	40	US-10-257-017B-343124	Sequence 2
C 963	8.4	70.0	42.0	12	40	US-10-257-017B-343306	Sequence 2
C 964	8.4	70.0	42.0	12	40	US-10-257-017B-344303	Sequence 2
C 965	8.4	70.0	42.0	12	40	US-10-257-017B-346809	Sequence 2
C 966	8.4	70.0	42.0	12	40	US-10-257-017B-347105	Sequence 2
C 967	8.4	70.0	42.0	12	40	US-10-257-017B-347106	Sequence 2
C 968	8.4	70.0	42.0	12	40	US-10-257-017B-347275	Sequence 2
C 969	8.4	70.0	42.0	12	40	US-10-257-017B-347597	Sequence 2
C 970	8.4	70.0	42.0	12	40	US-10-257-017B-348478	Sequence 2
C 971	8.4	70.0	42.0	12	40	US-10-257-017B-352722	Sequence 2
C 972	8.4	70.0	42.0	12	40	US-10-257-017B-352762	Sequence 2
C 973	8.4	70.0	42.0	12	40	US-10-257-017B-352880	Sequence 2
C 974	8.4	70.0	42.0	12	40	US-10-257-017B-353886	Sequence 2
C 975	8.4	70.0	42.0	12	40	US-10-257-017B-354932	Sequence 2
C 976	8.4	70.0	42.0	12	40	US-10-257-017B-355010	Sequence 2
C 977	8.4	70.0	42.0	12	40	US-10-257-017B-355310	Sequence 2
C 978	8.4	70.0	42.0	12	40	US-10-257-017B-358202	Sequence 2
C 979	8.4	70.0	42.0	12	40	US-10-257-017B-359017	Sequence 2
C 980	8.4	70.0	42.0	12	40	US-10-257-017B-359643	Sequence 2
C 981	8.4	70.0	42.0	12	40	US-10-257-017B-361463	Sequence 2
C 982	8.4	70.0	42.0	12	40	US-10-257-017B-361738	Sequence 2
C 983	8.4	70.0	42.0	12	40	US-10-257-017B-361979	Sequence 2
C 984	8.4	70.0	42.0	12	40	US-10-257-017B-362769	Sequence 2
C 985	8.4	70.0	42.0	12	40	US-10-257-017B-363267	Sequence 2
C 986	8.4	70.0	42.0	12	40	US-10-257-017B-363675	Sequence 2
C 987	8.4	70.0	42.0	12	40	US-10-257-017B-364075	Sequence 2
C 988	8.4	70.0	42.0	12	40	US-10-257-017B-364597	Sequence 2
C 989	8.4	70.0	42.0	12	40	US-10-257-017B-366105	Sequence 2
C 990	8.4	70.0	42.0	12	40	US-10-257-017B-366773	Sequence 2
C 991	8.4	70.0	42.0	12	40	US-10-257-017B-366978	Sequence 2
C 992	8.4	70.0	42.0	12	40	US-10-257-017B-367247	Sequence 2
C 993	8.4	70.0	42.0	12	40	US-10-257-017B-367323	Sequence 2
C 994	8.4	70.0	42.0	12	40	US-10-257-017B-369031	Sequence 2
C 995	8.4	70.0	42.0	12	40	US-10-257-017B-369031	Sequence 2
C 996	8.4	70.0	42.0	12	40	US-10-257-017B-369870	Sequence 2
C 997	8.4	70.0	42.0	12	40	US-10-257-017B-371399	Sequence 2
C 998	8.4	70.0	42.0	12	40	US-10-257-017B-371986	Sequence 2
C 999	8.4	70.0	42.0	12	40	US-10-257-017B-373586	Sequence 2
C 1000	8.4	70.0	42.0	12	40	US-10-257-017B-373586	Sequence 2

ALIGNMENTS

RESULT 1

PCT-US02-22417-64

Sequence 64, Application PC/TUS0222417

GENERAL INFORMATION:

APPLICANT: Hong Zhang

APPLICANT: Andrew T. Watt

APPLICANT: Isis Pharmaceuticals, Inc.

TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION

FILE REFERENCE: RTSP-0395

CURRENT APPLICATION NUMBER: PCT/US02/22417

CURRENT FILING DATE: 2002-07-13

PRIOR APPLICATION NUMBER: 09/908,147

PRIOR FILING DATE: 2001-07-17

NUMBER OF SEQ ID NOS: 168

SEQ ID NO 64

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

PCT-US02-22417-64

Query Match 100.0%; Score 20; DB 1; Length 20;

Score over Length 100.0%;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAGTTGCCGT 20

|||||

Db 1 GCCCCAGTTGAAGTTGCCGT 20

RESULT 2

US-09-908-147-64
; Sequence 64, Application US/09908147
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US09-908-147-64

Query Match 100.0%; Score 20; DB 34; Length 20;
Score over Length 100.0%;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCCGT 20
|||||
Db 1 GCCCCAGTTGAAGTTGCCGT 20

RESULT 3

US-10-728-509-64
; Sequence 64, Application US/10728509
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-64

Query Match 100.0%; Score 20; DB 56; Length 20;
Score over Length 100.0%;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCCGT 20
|||||
Db 1 GCCCCAGTTGAAGTTGCCGT 20

RESULT 4

PCT-US02-22417-65
; Sequence 65, Application PC/TUS0222417
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0395
; CURRENT APPLICATION NUMBER: PCT/US02/22417

; CURRENT FILING DATE: 2002-07-13
; PRIOR APPLICATION NUMBER: 09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-22417-65

Query Match 90.0%; Score 18; DB 1; Length 20;
Score over Length 90.0%;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCC 18
|||||
Db 3 GCCCCAGTTGAAGTTGCC 20

RESULT 5

US-09-908-147-65
; Sequence 65, Application US/09908147
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-65

Query Match 90.0%; Score 18; DB 34; Length 20;
Score over Length 90.0%;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCC 18
|||||
Db 3 GCCCCAGTTGAAGTTGCC 20

RESULT 6

US-10-728-509-65
; Sequence 65, Application US/10728509
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-65

Query Match 90.0%; Score 18; DB 56; Length 20;

Score over Length 90.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Mismatches 0;
Matches 18; Conservative 0;
QY 1 GCCCCAGTTGAAGTTGCC 18
Db 3 GCCCCAGTTGAAGTTGCC 20

RESULT 7
US-10-708-953-393940
; Sequence 393940, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 393940
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-393940

Query Match 57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1;
QY 1 GCCCCAGTTGAAG 13
Db 1 GCCCCACUUGAAG 13

RESULT 8
US-10-708-953-423956
; Sequence 423956, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 423956
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-423956

Query Match 57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1;
QY 1 GCCCCAGTTGAAG 13
Db 1 GCCCCACUUGAAG 13

RESULT 9
US-10-708-953-580710
; Sequence 580710, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036

; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580710
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-580710

Query Match 57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1;
QY 1 GCCCCAGTTGAAG 13
Db 1 GCCCCACUUGAAG 13

RESULT 10
US-10-708-953-801440
; Sequence 801440, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 801440
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-801440

Query Match 57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1;
QY 1 GCCCCAGTTGAAG 13
Db 1 GCCCCACUUGAAG 13

RESULT 11
US-10-708-953-1058146
; Sequence 1058146, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1058146
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1058146

Query Match 57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1;
QY 1 GCCCCAGTTGAAG 13
Db 1 GCCCCACUUGAAG 13

```
Db      1  GCCCCACUUGAAG 13

RESULT 12
US-10-708-953-1198625
; Sequence 1198625, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1198625
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1198625

Query Match      57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 13
US-10-708-953-2178793
; Sequence 2178793, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2178793
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2178793

Query Match      57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 14
US-10-708-953A-393940
; Sequence 393940, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 393940
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-393940

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 15
US-10-708-953A-423956
; Sequence 423956, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 423956
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-423956

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 16
US-10-708-953A-580710
; Sequence 580710, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 580710
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-580710

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 17
US-10-708-953A-801440
; Sequence 801440, Application US/10708953A
```

GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 801440
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-801440

Query Match 57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
||||| :|||
Db 1 GCCCCACUUGAAG 13

RESULT 18
US-10-708-953A-1058146
; Sequence 1058146, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1058146
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1058146

Query Match 57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
||||| :|||
Db 1 GCCCCACUUGAAG 13

GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1198625
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1198625

Query Match 57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;

Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
||||| :|||
Db 1 GCCCCACUUGAAG 13

RESULT 20
US-10-708-953A-2178793
; Sequence 2178793, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2178793
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2178793

Query Match 57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
||||| :|||
Db 1 GCCCCACUUGAAG 13

RESULT 21
PCT-US02-25942-1071/c
; Sequence 1071, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1071
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 157
PCT-US02-25942-1071

Query Match 65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
||||| :|||
Db 13 GCCCCAGTTGAAG 1

RESULT 22
PCT-US02-25942-1072
; Sequence 1072, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333

```

; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1072
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 156
PCT-US02-25942-1072

Query Match      65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 3 GCCCCAGTTGAAG 15

RESULT 23
PCT-US02-25942-1973/c
; Sequence 1973, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1973
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (2790547)...(2790562)
; OTHER INFORMATION: Chromosome = 3 Strand = positive ConnectronObjectNumber = 17163
PCT-US02-25942-1973

Query Match      65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 3 GCCCCAGTTGAAG 15

RESULT 24
US-10-227-567-1071/c
; Sequence 1071, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1071
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 157
US-10-227-567-1071

Query Match      65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 3 GCCCCAGTTGAAG 15

RESULT 25
US-10-227-567-1072
; Sequence 1072, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1072
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 156
US-10-227-567-1072

Query Match      65.0%; Score 13; DB 40; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 13 GCCCCAGTTGAAG 1

RESULT 26
US-10-227-567-1973/c
; Sequence 1973, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1973
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (2790547)...(2790562)
; OTHER INFORMATION: Chromosome = 3 Strand = positive ConnectronObjectNumber = 17163
US-10-227-567-1973

Query Match      65.0%; Score 13; DB 40; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 3 GCCCCAGTTGAAG 15

RESULT 27
US-10-367-729A-1071/c
; Sequence 1071, Application US/10367729A
```

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; LOCATION: (2790547)...(2790562)
; OTHER INFORMATION: Chromosome = 3 Strand = positive ConnectionObjectNumber = 17163
US-10-367-729A-1973

Query Match 65.0%; Score 13; DB 46; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 1 GCCCCAGTTGAAG 13
Db 13 GCCCCAGTTGAAG 1

RESULT 30
US-10-708-953-550673/c
; Sequence 550673, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 550673
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-550673

Query Match 52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 1;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 31
US-10-708-953-691520/c
; Sequence 691520, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 691520
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-691520

Query Match 52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 1;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 32
US-10-708-953-1007429/c
; Sequence 1007429, Application US/10708953

```

GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
FILE REFERENCE: 55036
CURRENT APPLICATION NUMBER: US/10/708,953
CURRENT FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 2254510
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1007429
LENGTH: 12
TYPE: RNA
ORGANISM: Homo sapiens
US-10-708-953-1007429

Query Match 52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 33
US-10-708-953-1161356/c
Sequence 1161356, Application US/10708953
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
FILE REFERENCE: 55036
CURRENT APPLICATION NUMBER: US/10/708,953
CURRENT FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 2254510
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1161356
LENGTH: 12
TYPE: RNA
ORGANISM: Homo sapiens
US-10-708-953-1161356

Query Match 52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 34
US-10-708-953-1293526/c
Sequence 1293526, Application US/10708953
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
FILE REFERENCE: 55036
CURRENT APPLICATION NUMBER: US/10/708,953
CURRENT FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 2254510
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1293526
LENGTH: 12
TYPE: RNA
ORGANISM: Homo sapiens
US-10-708-953-1293526

Query Match 52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;

Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 35
US-10-708-953-1483914/c
Sequence 1483914, Application US/10708953
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
FILE REFERENCE: 55036
CURRENT APPLICATION NUMBER: US/10/708,953
CURRENT FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 2254510
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1483914
LENGTH: 12
TYPE: RNA
ORGANISM: Homo sapiens
US-10-708-953-1483914

Query Match 52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 36
US-10-708-953-1637846/c
Sequence 1637846, Application US/10708953
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
FILE REFERENCE: 55036
CURRENT APPLICATION NUMBER: US/10/708,953
CURRENT FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 2254510
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1637846
LENGTH: 12
TYPE: RNA
ORGANISM: Homo sapiens
US-10-708-953-1637846

Query Match 52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 37
US-10-708-953-1982721/c
Sequence 1982721, Application US/10708953
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
FILE REFERENCE: 55036
CURRENT APPLICATION NUMBER: US/10/708,953


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; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1982721
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1982721

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 38
US-10-708-953A-550673/c
; Sequence 550673, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 550673
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-550673

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 39
US-10-708-953A-691520/c
; Sequence 691520, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 691520
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-691520

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 40
US-10-708-953A-1007429/c
; Sequence 1007429, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1007429
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1007429

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 41
US-10-708-953A-1161356/c
; Sequence 1161356, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1161356
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1161356

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 42
US-10-708-953A-1293526/c
; Sequence 1293526, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1293526
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1293526
```

```
; ORGANISM: Homo sapiens
US-10-708-953A-1293526

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
    ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 43
US-10-708-953A-1483914/c
; Sequence 1483914, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1483914
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1483914

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
    ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 44
US-10-708-953A-1637846/c
; Sequence 1637846, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1637846
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1637846

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
    ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 45
US-10-708-953A-1982721/c
; Sequence 1982721, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1982721
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1982721

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
    ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 46
PCT-US07-68401-1552/c
; Sequence 1552, Application PC/TUS0768401
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric B. Swayze
; APPLICANT: Edward Wanczewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: PCT/US07/68401
; CURRENT FILING DATE: 2007-05-25
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68401-1552

Query Match      60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
    ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 47
```

PCT-US07-68403-1552/c
; Sequence 1552, Application PC/TUS0768402
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W015
; CURRENT APPLICATION NUMBER: PCT/US07/68402
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68402-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 48
PCT-US07-68403-1552/c
; Sequence 1552, Application PC/TUS0768403
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W08
; CURRENT APPLICATION NUMBER: PCT/US07/68403
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68402-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 48
PCT-US07-68403-1552/c
; Sequence 1552, Application PC/TUS0768403
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W08
; CURRENT APPLICATION NUMBER: PCT/US07/68403
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68402-1552

PCT-US07-68403-1552
; Sequence 1552, Application PC/TUS0768403
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W010
; CURRENT APPLICATION NUMBER: PCT/US07/68404
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68404-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 49
PCT-US07-68404-1552/c
; Sequence 1552, Application PC/TUS0768404
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W010
; CURRENT APPLICATION NUMBER: PCT/US07/68404
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68404-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 50
PCT-US07-68406-1552/c
; Sequence 1552, Application PC/TUS0768406

```
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punith P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF SGLT2
; CURRENT APPLICATION NUMBER: PCT/US07/68406
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68406-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 51
PCT-US07-68408-1552/c
; Sequence 1552, Application PC/TUS0768408
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punith P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF CRP
; CURRENT APPLICATION NUMBER: PCT/US07/68408
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68406-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 51
PCT-US07-68408-1552/c
; Sequence 1552, Application PC/TUS0768408
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punith P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF CRP
; CURRENT APPLICATION NUMBER: PCT/US07/68408
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
```

```
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68408-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 52
PCT-US07-68410-1552/c
; Sequence 1552, Application PC/TUS0768410
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punith P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF GCCR
; CURRENT APPLICATION NUMBER: PCT/US07/68410
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68410-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 53
PCT-US07-68412-1552/c
; Sequence 1552, Application PC/TUS0768412
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
```

APPLICANT: Sanjay Bhanot
APPLICANT: Richard S. Geary
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Punit P. Seth
APPLICANT: Andrew M. Siwkowski
APPLICANT: Eric E. Swayze
APPLICANT: Edward Wancewitz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: EXPRESSION OF GCGR
FILE REFERENCE: CORE0061W013
CURRENT APPLICATION NUMBER: PCT/US07/68412
CURRENT FILING DATE: 2007-05-25
PRIOR APPLICATION NUMBER: PCT/US2007/061183
PRIOR FILING DATE: 2007-01-27
PRIOR APPLICATION NUMBER: 60/746,631
PRIOR FILING DATE: 2006-05-05
PRIOR APPLICATION NUMBER: 60/747,059
PRIOR FILING DATE: 2006-05-11
PRIOR APPLICATION NUMBER: 60/805,660
PRIOR FILING DATE: 2006-06-23
PRIOR APPLICATION NUMBER: 60/864,554
PRIOR FILING DATE: 2006-11-06
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1552
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68412-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 54
US-11-745-429-1552/c
Sequence 1552, Application US/11745429
GENERAL INFORMATION:
APPLICANT: Sanjay Bhanot
APPLICANT: Richard S. Geary
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Punit P. Seth
APPLICANT: Andrew M. Siwkowski
APPLICANT: Eric E. Swayze
APPLICANT: Edward Wancewitz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: GENE EXPRESSION
FILE REFERENCE: CORE0061US7
CURRENT APPLICATION NUMBER: US/11745,429
CURRENT FILING DATE: 2007-05-25
PRIOR APPLICATION NUMBER: PCT/US2007/061183
PRIOR FILING DATE: 2007-01-27
PRIOR APPLICATION NUMBER: 60/746,631
PRIOR FILING DATE: 2006-05-05
PRIOR APPLICATION NUMBER: 60/747,059
PRIOR FILING DATE: 2006-05-11
PRIOR APPLICATION NUMBER: 60/805,660
PRIOR FILING DATE: 2006-06-23
PRIOR APPLICATION NUMBER: 60/864,554
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1552

LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-11-745-429-1552

Query Match 60.0%; Score 12; DB 81; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 55
PCT-US02-22417-5
Sequence 5, Application PC/TUS0222417
GENERAL INFORMATION:
APPLICANT: Hong Zhang
APPLICANT: Andrew T. Watt
APPLICANT: Isis Pharmaceuticals, Inc.
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
FILE REFERENCE: RTSP-0395
CURRENT APPLICATION NUMBER: PCT/US02/22417
CURRENT FILING DATE: 2002-07-13
PRIOR APPLICATION NUMBER: 09/908,147
PRIOR FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 5
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
PCT-US02-22417-5

Query Match 75.0%; Score 15; DB 1; Length 18;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15
Db 4 GCCCCAGTTGAAGTT 18

RESULT 56
US-09-908-147-5
Sequence 5, Application US/09908147
GENERAL INFORMATION:
APPLICANT: Hong Zhang
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
FILE REFERENCE: RTS-0185
CURRENT APPLICATION NUMBER: US/09/908,147
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 5
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-908-147-5

Query Match 75.0%; Score 15; DB 34; Length 18;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15
|||||
Db 4 GCCCCAGTTGAAGTT 18

RESULT 57

US-10-728-509-5
; Sequence 5, Application US/10728509
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-728-509-5

Query Match 75.0%; Score 15; DB 56; Length 18;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15
|||||
Db 4 GCCCCAGTTGAAGTT 18

RESULT 58

US-10-257-017B-271773/c
; Sequence 271773, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 271773
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002613
US-10-257-017B-271773

Query Match 50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACTTGAAGTT 15
|||||
Db 10 ACTTGAAGTT 1

RESULT 59

US-10-257-017B-274756/c
; Sequence 274756, Application US/10257017B
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 274756
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003668
US-10-257-017B-274756

Query Match 50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTT 15
|||||
Db 10 AGTTGAAGTT 1

RESULT 60

US-10-257-017B-310208
; Sequence 310208, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310208
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863
US-10-257-017B-310208

Query Match 50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GTTGAAGTTG 16
|||||
Db 1 GTTGAAGTTG 10

RESULT 61

US-10-257-017B-341473/c
; Sequence 341473, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341473
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042053
US-10-257-017B-341473

Query Match      50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      11 AGTTGAAGTT 2

RESULT 62
US-10-257-017B-353251
; Sequence 353251, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353251
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048401
US-10-257-017B-353251

Query Match      50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      1 AGTTGAAGTT 10

RESULT 63
US-10-257-017B-355811/c
; Sequence 355811, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355811
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049826
US-10-257-017B-355811

Query Match      50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGAAGTT 1

RESULT 64
PCT-US02-22417-119
; Sequence 119, Application PC/TUS0222417
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTSP-0395
; CURRENT APPLICATION NUMBER: PCT/US02/22417
; CURRENT FILING DATE: 2002-07-13
; PRIOR APPLICATION NUMBER: 09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-22417-119

Query Match      82.0%; Score 16.4; DB 1; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAGTTGCCGT 20
Db      1 CCCAGTTGAAGTTGCCAT 18

RESULT 65
US-09-908-147-119
; Sequence 119, Application US/09908147
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-119

Query Match      82.0%; Score 16.4; DB 34; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAGTTGCCGT 20
Db      119
```

Db 1 CCAGTTGAAGTTGCCAT 18

RESULT 66
US-10-728-509-119
; Sequence 119, Application US/10728509
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-119

Query Match 82.0%; Score 16.4; DB 56; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCAGTTGAAGTTGCCGT 20
|||||

Db 1 CCAGTTGAAGTTGCCAT 18
|||||

RESULT 67
US-08-591-486B-33
; Sequence 33, Application US/08591486B
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg F
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Gotingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
; TITLE OF INVENTION: Treatment of Neoplasms
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-9350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-33

Query Match 57.0%; Score 11.4; DB 14; Length 14;
Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 7.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
|||||

Db 2 GTTGAAGTTGCTG 14
|||||

RESULT 68
US-08-591-486C-33
; Sequence 33, Application US/08591486C
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg F
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Gotingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition Comprising Antisense-Nucleic Acid for
; TITLE OF INVENTION: Prevention and/or Treatment of Neuronal Injury, Degeneration and
; TITLE OF INVENTION: for the Treatment of Neoplasms
; FILE REFERENCE: P60122
; CURRENT APPLICATION NUMBER: US/08/591,486C
; CURRENT FILING DATE: 1996-01-11
; PRIOR APPLICATION NUMBER: PCT/EP94/02218
; PRIOR FILING DATE: 1994-07-06
; PRIOR APPLICATION NUMBER: EP 93111059.7
; PRIOR FILING DATE: 1993-07-10
; NUMBER OF SEQ ID NOS: 186
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Antisense nucleic acid
US-08-591-486C-33

Query Match 57.0%; Score 11.4; DB 14; Length 14;
Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 7.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
|||||

Db 2 GTTGAAGTTGCTG 14
|||||

RESULT 69
US-10-708-953-393713
; Sequence 393713, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 393713


```
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-393713

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 70
US-10-708-953-445749
; Sequence 445749, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 445749
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-445749

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 71
US-10-708-953-591846
; Sequence 591846, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 591846
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-591846

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 72
US-10-708-953-783771
; Sequence 783771, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 783771
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-783771

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 73
US-10-708-953-1022044
; Sequence 1022044, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1022044
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1022044

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 74
US-10-708-953-1241906
; Sequence 1241906, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1241906
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1241906

Query Match      57.0%; Score 11.4; DB 52; Length 14;
```

```
Score over Length      81.4%;      Pred. No. 7.8e+05;
Best Local Similarity  76.9%;      2; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 75
US-10-708-953-1832566
; Sequence 1832566, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1832566
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1832566

Query Match      57.0%;      Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 76
US-10-708-953A-393713
; Sequence 393713, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 393713
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-393713

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 77
US-10-708-953A-445749
; Sequence 445749, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
```

```
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 445749
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-445749

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 78
US-10-708-953A-591846
; Sequence 591846, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 591846
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-591846

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 79
US-10-708-953A-783771
; Sequence 783771, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 783771
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-783771

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 2 GCCCCACUUGAAG 14
```

```
Db      2 GCCCCACUUGAAG 14

RESULT 80
US-10-708-953A-1022044
; Sequence 1022044, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1022044
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1022044

Query Match      57.0%; Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAAG 13
        ||||| :|||
Db      2 GCCCCACUUGAAG 14

RESULT 81
US-10-708-953A-1241906
; Sequence 1241906, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1241906
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1241906

Query Match      57.0%; Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAAG 13
        ||||| :|||
Db      2 GCCCCACUUGAAG 14

RESULT 82
US-10-708-953A-1832566
; Sequence 1832566, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1832566
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1832566

Query Match      57.0%; Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAAG 13
        ||||| :|||
Db      2 GCCCCACUUGAAG 14

RESULT 83
US-10-984-919-857
; Sequence 857, Application US/10984919
; GENERAL INFORMATION:
; APPLICANT: Schlengerslepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 857
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-857

Query Match      57.0%; Score 11.4; DB 60; Length 14;
Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 7.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCCG 19
        ||||| :|||
Db      2 GTTGAAGTTGCTG 14

RESULT 84
US-10-594-448-16
; Sequence 16, Application US/10594448
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, Akira
; APPLICANT: OZAKI, Toshihori
; TITLE OF INVENTION: METHOD OF SCREENING COMPOUND CAPABLE OF ACCELERATING OR INHIBITING
; TITLE OF INVENTION: APOPTOSIS, APOPTOSIS ACCELERATOR AND APOPTOSIS INHIBITOR
; FILE REFERENCE: Q97365
; CURRENT APPLICATION NUMBER: US/10/594,448
; CURRENT FILING DATE: 2006-09-26
; PRIOR APPLICATION NUMBER: JP 2004-93,266
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: JP 2004-176,107
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
```

; OTHER INFORMATION: primer for Bax
US-10-594-448-16

Query Match 80.0%; Score 16; DB 48; Length 20;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
|||||
Db 1 CAGTTGAAGTTGCCGT 16

RESULT 85

US-09-708-690-4126/c
; Sequence 4126, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-708-690-4126

Query Match 60.0%; Score 12; DB 30; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAGT 14
|||||
Db 15 CCAGTTGAAGT 4

RESULT 86

US-09-870-161-4126/c
; Sequence 4126, Application US/09870161
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-W (400/026)
; CURRENT APPLICATION NUMBER: US/09/870,161
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 20821
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-870-161-4126

Query Match 60.0%; Score 12; DB 33; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAGT 14
|||||
Db 15 CCAGTTGAAGT 4

RESULT 87

US-10-287-949A-4126/c
; Sequence 4126, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4126

Query Match 60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAGT 14
|||||
Db 15 CCAGTTGAAGT 4

RESULT 88

US-10-287-949B-4126/c
; Sequence 4126, Application US/10287949B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 00-876-O (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949B
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949B-4126

Query Match 60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAGT 14
|||||

```
Db      15 CCCAGTTGAAGT 4

RESULT 89
US-10-287-949C-4126/c
; Sequence 4126, Application US/10287949C
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 00-876-O (400/053)
; CURRENT APPLICATION NUMBER: US/10/287,949C
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949C-4126

Query Match      60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAGT 14
      ||| ||||| ||||| |||||
Db      15 CCCAGTTGAAGT 4

RESULT 90
US-10-294-038-5264/c
; Sequence 5264, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 5264
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (2313785)...(2313798)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6574
US-10-294-038-5264

Query Match      60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
      ||| ||||| ||||| |||||
Db      15 AGTTGAAGTTGC 4

RESULT 91
US-10-294-038A-5264/c
; Sequence 5264, Application US/10294038A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038A
```

```
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 5264
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (2313785)...(2313798)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6574
US-10-294-038A-5264

Query Match      60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
      ||| ||||| ||||| |||||
Db      15 AGTTGAAGTTGC 4

RESULT 92
US-10-951-303-4126/c
; Sequence 4126, Application US/10951303
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-4126

Query Match      60.0%; Score 12; DB 60; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAGT 14
      ||| ||||| ||||| |||||
Db      15 CCCAGTTGAAGT 4

RESULT 93
US-10-951-303B-4126/c
; Sequence 4126, Application US/10951303B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
```

FILE REFERENCE: 400/158 (MBH00-876-P)
CURRENT APPLICATION NUMBER: US/10/951,303B
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US 09/685,664
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8228
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4126
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-951-303B-4126

Query Match 60.0%; Score 12; DB 60; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||||
DB 15 CCCAGTTGAAGT 4

RESULT 94
US-11-088-219-4126/c
Sequence 4126, Application US/11088219
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
TITLE OF INVENTION: (VEGF-R)
FILE REFERENCE: MBH00-876-Q (400/266)
CURRENT APPLICATION NUMBER: US/11/088,219
CURRENT FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: 10/138,674
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 09/870,161
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 09/708,690
PRIOR FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: 09/371,722
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 08/584,040
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/005,974
PRIOR FILING DATE: 1995-10-26
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4126
LENGTH: 15
TYPE: RNA
ORGANISM: Homo sapiens
US-11-088-219-4126

Query Match 60.0%; Score 12; DB 63; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||||
DB 15 CCCAGTTGAAGT 4

RESULT 95

US-11-088-219A-4126/c
Sequence 4126, Application US/11088219A
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
TITLE OF INVENTION: Conditions
TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: 400/266 (MBH00-876-0)
CURRENT APPLICATION NUMBER: US/11/088,219A
CURRENT FILING DATE: 2005-03-23
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4126
LENGTH: 15
TYPE: RNA
ORGANISM: Homo sapiens
US-11-088-219A-4126

Query Match 60.0%; Score 12; DB 63; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||||
DB 15 CCCAGTTGAAGT 4

RESULT 96

US-10-257-017B-187031
Sequence 187031, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 187031
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187031

Query Match 52.0%; Score 10.4; DB 40; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
|||||
DB 1 AGTTGAAGTTGC 12

RESULT 97

US-10-257-017B-187032/c
Sequence 187032, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187032
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187032

Query Match      52.0%; Score 10.4; DB 40; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCGC 17
Db      13 AGTTGAAGTTGCGC 2

RESULT 98
PCT-US06-29646A-94101
; Sequence 94101, Application PC/TUS0629646A
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAS AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: PCT/US06/29646A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94101
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
PCT-US06-29646A-94101

Query Match      67.0%; Score 13.4; DB 3; Length 17;
Score over Length 78.8%;
Best Local Similarity 93.3%; Pred. No. 7.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCGC 20
Db      3 AGTTGAAGTTGCGC 17

RESULT 99
PCT-US06-29646A-94101
; Sequence 94101, Application US/11495951A
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAS AND METHODS OF USE
; FILE REFERENCE: 99689-00009
```

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; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94101
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-94101
```

```
Query Match      67.0%; Score 13.4; DB 77; Length 17;
Score over Length 78.8%;
Best Local Similarity 93.3%; Pred. No. 7.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCGC 20
Db      3 AGTTGAAGTTGCGC 17
```

```
RESULT 100
PCT-US07-68401-1116/c
; Sequence 1116, Application PC/TUS0768401
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanczewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: PCT/US07/68401
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68401-1116
```

```
Query Match      47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      12 AGTTGAAGTTG 2

RESULT 101
```

PCT-US07-68402-1116/c
; Sequence 1116, Application PC/TUS0768402
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanczewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W015
; CURRENT APPLICATION NUMBER: PCT/US07/68402
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68402-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 12 AGTTGGAGTTG 2

RESULT 102
PCT-US07-68403-1116/c
; Sequence 1116, Application PC/TUS0768403
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanczewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W08
; CURRENT APPLICATION NUMBER: PCT/US07/68403
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68403-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 12 AGTTGGAGTTG 2

RESULT 103
PCT-US07-68404-1116/c
; Sequence 1116, Application PC/TUS0768404
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanczewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W010
; CURRENT APPLICATION NUMBER: PCT/US07/68404
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68404-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 12 AGTTGGAGTTG 2

RESULT 104
PCT-US07-68406-1116/c
; Sequence 1116, Application PC/TUS0768406

PCT-US07-68402-1116/c
; Sequence 1116, Application PC/TUS0768402
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanczewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W015
; CURRENT APPLICATION NUMBER: PCT/US07/68402
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68403-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 12 AGTTGGAGTTG 2

RESULT 103
PCT-US07-68404-1116/c
; Sequence 1116, Application PC/TUS0768404
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanczewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W010
; CURRENT APPLICATION NUMBER: PCT/US07/68404
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68404-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 12 AGTTGGAGTTG 2

RESULT 104
PCT-US07-68406-1116/c
; Sequence 1116, Application PC/TUS0768406


```
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF SGLT2
; FILE REFERENCE: CORE0061W09
; CURRENT APPLICATION NUMBER: PCT/US07/68406
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68406-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGGAGTTG 2

RESULT 105
PCT-US07-68408-1116/c
; Sequence 1116, Application PC/TUS0768408
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF CRP
; FILE REFERENCE: CORE0061W011
; CURRENT APPLICATION NUMBER: PCT/US07/68408
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
```

```
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68408-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGGAGTTG 2

RESULT 106
PCT-US07-68410-1116/c
; Sequence 1116, Application PC/TUS0768410
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF GCCR
; FILE REFERENCE: CORE0061W012
; CURRENT APPLICATION NUMBER: PCT/US07/68410
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68410-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGGAGTTG 2

RESULT 107
PCT-US07-68412-1116/c
; Sequence 1116, Application PC/TUS0768412
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
```

APPLICANT: Sanjay Bhanot
APPLICANT: Richard S. Geary
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Punit P. Seth
APPLICANT: Andrew M. Siwkowski
APPLICANT: Eric E. Swayze
APPLICANT: Edward Wanczewitz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: EXPRESSION OF GCCR
FILE REFERENCE: CORE061W013
CURRENT APPLICATION NUMBER: PCT/US07/68412
CURRENT FILING DATE: 2007-05-25
PRIOR APPLICATION NUMBER: PCT/US2007/061183
PRIOR FILING DATE: 2007-01-27
PRIOR APPLICATION NUMBER: 60/746,631
PRIOR FILING DATE: 2006-05-05
PRIOR APPLICATION NUMBER: 60/747,059
PRIOR FILING DATE: 2006-05-11
PRIOR APPLICATION NUMBER: 60/805,660
PRIOR FILING DATE: 2006-06-23
PRIOR APPLICATION NUMBER: 60/864,554
PRIOR FILING DATE: 2006-11-06
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1116
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68412-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 12 AGTTGAAGTTG 2

RESULT 108
PCT-US98-26935-370/c
Sequence 370, Application PC/TUS9826935
GENERAL INFORMATION:
APPLICANT: Jessen, Holly
APPLICANT: Webb, David
APPLICANT: Coryell, Virginia H.
APPLICANT: Schupp, James M.
APPLICANT: Keim, Paul S.
APPLICANT: Pioneer Hi-Bred International, Inc.
TITLE OF INVENTION: Nucleotide Polymorphisms in Soybean
FILE REFERENCE: 018574-000110PC
CURRENT APPLICATION NUMBER: PCT/US98/26935
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: US 60/068,185
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 795
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 370
LENGTH: 12
TYPE: DNA
ORGANISM: Glycine max
PCT-US98-26935-370

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14

DB 11 CCAGTTGAAGT 1

RESULT 109
US-09-215-436-370/c
Sequence 370, Application US/09215436
GENERAL INFORMATION:
APPLICANT: Jessen, Holly
APPLICANT: Webb, David
APPLICANT: Coryell, Virginia H.
APPLICANT: Schupp, James M.
APPLICANT: Keim, Paul S.
APPLICANT: Pioneer Hi-Bred International, Inc.
TITLE OF INVENTION: Nucleotide Polymorphisms in Soybean
FILE REFERENCE: 018574-000110US
CURRENT APPLICATION NUMBER: US/09/215,436
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: US 60/068,185
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 795
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 370
LENGTH: 12
TYPE: DNA
ORGANISM: Glycine max
US-09-215-436-370

Query Match 47.0%; Score 9.4; DB 21; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
DB 11 CCAGTTGAAGT 1

RESULT 110
US-09-581-970A-370/c
Sequence 370, Application US/09581970A
GENERAL INFORMATION:
APPLICANT: JESSEN, HOLLY
APPLICANT: WEBB, DAVID
APPLICANT: CORYELL, VIRGINIA H.
APPLICANT: SCHUPP, JAMES M.
APPLICANT: KEIM, PAUL S.
TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
FILE REFERENCE: 04-000111US
CURRENT APPLICATION NUMBER: US/09/581,970A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: PCT/US98/26935
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/068,185
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 798
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 370
LENGTH: 12
TYPE: DNA
ORGANISM: Glycine max
US-09-581-970A-370

Query Match 47.0%; Score 9.4; DB 26; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
DB 11 CCAGTTGAAGT 1

```
RESULT 111
US-10-257-017B-275133/c
; Sequence 275133, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 275133
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003795
US-10-257-017B-275133

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGAGTTG 2

RESULT 112
US-10-257-017B-280261
; Sequence 280261, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280261
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008409
US-10-257-017B-280261

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 1 AGTTGAAGTTG 11

RESULT 113
US-10-257-017B-281972/c
; Sequence 281972, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010216
US-10-257-017B-281972

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 11 AGTTGATGTTG 1

RESULT 114
US-10-257-017B-282569/c
; Sequence 282569, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 282569
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010870
US-10-257-017B-282569

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGATGTTG 2

RESULT 115
US-10-257-017B-300630
; Sequence 300630, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300630
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019120
US-10-257-017B-300630

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
Db 2 AGTTGAAGTTG 12

RESULT 116

US-10-257-017B-305246
; Sequence 305246, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305246
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021354
US-10-257-017B-305246

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
Db 2 AGTTGATGTTG 12

RESULT 117

US-10-257-017B-314348
; Sequence 314348, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314348
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026294
US-10-257-017B-314348

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-257-017B-314348

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
Db 2 AGTTAAAGTTG 12

RESULT 118

US-10-257-017B-329434
; Sequence 329434, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329434
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034943
US-10-257-017B-329434

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
Db 1 AGTAGAAGTTG 11

RESULT 119

US-10-257-017B-337757
; Sequence 337757, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337757
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004732
US-10-257-017B-337757

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 1 AGTGAAGTTG 11

RESULT 120
US-10-257-017B-339358/c
; Sequence 339358, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 339358
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040958
US-10-257-017B-339358

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 11 AATTGAAGTTG 1

RESULT 121
US-10-257-017B-345090/c
; Sequence 345090, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 345090
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043868
US-10-257-017B-345090

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 11 AGTTGAGTTG 1

RESULT 122
US-10-257-017B-361423

; Sequence 361423, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 361423
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052630
US-10-257-017B-361423

Query Match 47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 1 AGTTGAAGTTG 11

RESULT 123
US-10-708-952A-226611
; Sequence 226611, Application US/10708952A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 226611
; LENGTH: 12
; TYPE: RNA
; ORGANISM: JC virus
; OTHER INFORMATION:
US-10-708-952A-226611

Query Match 47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06; Indels 1; Gaps 0;
Matches 6; Conservative 4; Mismatches 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTT 15
Db 1 CAGUUGCAGUU 11

RESULT 124
US-10-708-952A-365157
; Sequence 365157, Application US/10708952A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 365157
; LENGTH: 12

```
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952A-365157

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 125
US-10-708-952B-226611
; Sequence 226611, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 226611
; LENGTH: 12
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952B-226611

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 126
US-10-708-952B-365157
; Sequence 365157, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 365157
; LENGTH: 12
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952B-365157

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 127
US-10-708-952B-365157
; Sequence 365157, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 365157
; LENGTH: 12
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952B-365157

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 128
US-10-708-953-675075
; Sequence 675075, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 675075
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-675075

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12

RESULT 129
US-10-708-953-820071
; Sequence 820071, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 820071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-820071

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12

RESULT 130
US-10-708-953-820071
; Sequence 820071, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 820071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-820071

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12
```

```
US-10-708-953-425654
; Sequence 425654, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 425654
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-425654

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12

RESULT 131
US-10-708-953-675075
; Sequence 675075, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 675075
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-675075

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12

RESULT 132
US-10-708-953-820071
; Sequence 820071, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 820071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-820071

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12
```

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; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1160477
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1160477

Query Match          47.0%; Score 9.4; DB 52; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      11 AGTTCAGTTG 1

RESULT 133
US-10-708-953-1217858/c
; Sequence 1217858, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1217858
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1217858

Query Match          47.0%; Score 9.4; DB 52; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.3%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
Db      12 CCAGATGAAGT 2

RESULT 134
US-10-708-953-1458682/c
; Sequence 1458682, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1458682
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1458682

Query Match          47.0%; Score 9.4; DB 52; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14

```

```
Db      12 CCAGATGAAGT 2
||||| |||||
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2131356

RESULT 135
US-10-708-953-2070413
; Sequence 2070413, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2070413
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2070413

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCAGTTGA 11
||||| :||
Db 2 GCCCAGCUGA 12

RESULT 136
US-10-708-953-2110468/c
; Sequence 2110468, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2110468
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2110468

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCAGTTGA 11
||||| :||
Db 2 GCCCAGCUGA 12

RESULT 137
US-10-708-953-2131356/c
; Sequence 2131356, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2131356

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTCAGTTG 16
||||| |||||
Db 11 AGTTCAGTTG 11

RESULT 138
US-10-708-953-2226422/c
; Sequence 2226422, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2226422
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2226422

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTCAAGTTGC 17
||||| |||||
Db 12 GTTCAAGTTGC 2

RESULT 139
US-10-708-953A-425654
; Sequence 425654, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 425654
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-425654

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCAGTTGA 11
||||| :||
Db 2 GCCCAGCUGA 12

RESULT 140
US-10-708-953A-675075
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; Sequence 675075, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 675075
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-675075

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGA 11
Db 2 GCCCCAGCUGA 12

RESULT 141
US-10-708-953A-820071
; Sequence 820071, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 820071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-820071

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGA 11
Db 2 GCCCCAGCUGA 12

RESULT 142
US-10-708-953A-1049802
; Sequence 1049802, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1049802
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1049802

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGA 11
Db 2 GCCCCAGCUGA 12

RESULT 143
US-10-708-953A-1146690/c
; Sequence 1146690, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1146690
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1146690

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTCAAGTTGC 17
Db 12 GTTCAAGTTGC 2

RESULT 144
US-10-708-953A-1160477/c
; Sequence 1160477, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1160477
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1160477

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 11 AGTTGACGTTG 1

RESULT 145
US-10-708-953A-1217858/c
; Sequence 1217858, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
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; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1217858
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1217858

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
    ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 146
US-10-708-953A-1458682/c
; Sequence 1458682, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1458682
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1458682

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
    ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 147
US-10-708-953A-2070413
; Sequence 2070413, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2070413
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2070413

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
    ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 148
US-10-708-953A-2110468/c
; Sequence 2110468, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2110468
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2110468

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
    ||||| |||||
Db 11 AGTTGAGTTG 1

RESULT 149
US-10-708-953A-2131356/c
; Sequence 2131356, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2131356
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2131356

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
    ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 150
US-10-708-953A-2226422/c
; Sequence 2226422, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2226422
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2226422

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
    ||||| |||||
Db 12 CCAGATGAAGT 2
```

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2226422

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGC 17
   ||| |||||
Db 12 GTTCAAGTTCC 2

RESULT 151
US-10-709-572-155258
; Sequence 155258, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 155258
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-155258

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
   ||| |||||
Db 1 ACTTGAAGTTG 11

RESULT 152
US-10-709-572-186135
; Sequence 186135, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 186135
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-186135

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
   ||| |||||
Db 2 ACTTGAAGTTG 12

RESULT 153
US-10-709-572-269838
; Sequence 269838, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 269838
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-269838

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTT 15
   ||| |||||
Db 2 CTGTTGAAGTT 12

RESULT 154
US-11-745-429-1116/c
; Sequence 1116, Application US/11745429
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: US/11/745,429
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-11-745-429-1116

Query Match      47.0%; Score 9.4; DB 81; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGAAGTTG 2

RESULT 155

PCT-US02-25943-54229
; Sequence 54229, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 54229
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5299838)...(5299853)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 58096

PCT-US02-25943-54229

Query Match 62.0%; Score 12.4; DB 1; Length 16;
Score over Length 77.5%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 1 GGTGAAGTTGCCGT 14

RESULT 156

US-10-227-565-54229
; Sequence 54229, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 54229
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5299838)...(5299853)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 58096

US-10-227-565-54229

Query Match 62.0%; Score 12.4; DB 40; Length 16;
Score over Length 77.5%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 1 GGTGAAGTTGCCGT 14

RESULT 157

US-10-367-832A-54229
; Sequence 54229, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A

; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 54229
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5299838)...(5299853)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 58096

US-10-367-832A-54229

Query Match 62.0%; Score 12.4; DB 46; Length 16;
Score over Length 77.5%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 1 GGTGAAGTTGCCGT 14

RESULT 158

US-10-471-899-5/c
; Sequence 5, Application US/10471899
; GENERAL INFORMATION:
; APPLICANT: Diamond, Michael P.
; TITLE OF INVENTION: METHOD OF PREVENTING ADHESIONS BY APOPTOSIS OF ADHESION
; TITLE OF INVENTION: PERTONEAL CELLS
; FILE REFERENCE: DIAM-P01-002
; CURRENT APPLICATION NUMBER: US/10/471,899
; CURRENT FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: PCT/US02/07119
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.4
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-471-899-5

Query Match 85.0%; Score 17; DB 47; Length 22;
Score over Length 77.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCCGT 20
Db 22 CCAGTTGAAGTTGCCGT 6

RESULT 159

US-10-708-953-528084/c
; Sequence 528084, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 528084
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-528084

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;

```
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   ||| ||| ||| |||
Db 14 CAGGTGAAGTGCC 1

RESULT 160
US-10-708-953-613923
; Sequence 613923, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 613923
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-613923

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
   ||| ||| ||| |||
Db 1 GUUGAAGUGCCAU 14

RESULT 161
US-10-708-953-668724
; Sequence 668724, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 668724
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-668724

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGT 14
   ||| ||| ||| |||
Db 1 GCCCAAGUUGCAGU 14

RESULT 162
US-10-708-953-1269719/c
; Sequence 1269719, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
```

```
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1269719
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1269719

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   ||| ||| ||| |||
Db 14 CAGGTGAAGTGCC 1

RESULT 163
US-10-708-953-1475347/c
; Sequence 1475347, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1475347
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1475347

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   ||| ||| ||| |||
Db 14 CAGGTGAAGTGCC 1

RESULT 164
US-10-708-953-1713144/c
; Sequence 1713144, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1713144
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1713144

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   ||| ||| ||| |||
Db 14 CAGGTGAAGTGCC 1
```

```
RESULT 165
US-10-708-953-1883139
; Sequence 1883139, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1883139
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1883139

Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAAGT 14
DB 1 GCCCAGUUGCAGU 14

RESULT 166
US-10-708-953-1898598
; Sequence 1898598, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1898598
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1898598

Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAAGT 14
DB 1 GCCCAGUUGCAGU 14

RESULT 167
US-10-708-953-2077386/c
; Sequence 2077386, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2077386
; LENGTH: 14
; TYPE: RNA
US-10-708-953-2077386/c

Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
DB 1 GUUGAAGGUGGCCAU 14

RESULT 168
US-10-708-953A-528084/c
; Sequence 528084, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 528084
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-528084

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGGTGCC 1

RESULT 169
US-10-708-953A-613923
; Sequence 613923, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 613923
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-613923

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGGTGCC 1

RESULT 170
US-10-708-953A-668724
; Sequence 668724, Application US/10708953A
; GENERAL INFORMATION:
```

```
; ORGANISM: Homo sapiens
US-10-708-953-2077386
```

```
Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGGTGCC 1
```

```
RESULT 168
US-10-708-953A-528084/c
; Sequence 528084, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 528084
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-528084
```

```
Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGGTGCC 1
```

```
RESULT 169
US-10-708-953A-613923
; Sequence 613923, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 613923
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-613923
```

```
Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
DB 1 GUUGAAGGUGGCCAU 14
```

```
RESULT 170
US-10-708-953A-668724
; Sequence 668724, Application US/10708953A
; GENERAL INFORMATION:
```

```
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 668724
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-668724

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCGAGTTGAAGT 14
   |||||:::|
Db 1 GCCCAAGUUGCAGU 14

RESULT 171
US-10-708-953A-1269719/c
; Sequence 1269719, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1269719
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1269719

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 1

RESULT 172
US-10-708-953A-1475347/c
; Sequence 1475347, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1475347
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1475347

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 1

RESULT 173
US-10-708-953A-1883139
; Sequence 1883139, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1883139
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1883139

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCGAGTTGAAGT 14
   |||||:::|
Db 1 GCCCAAGUUGCAGU 14

RESULT 175
US-10-708-953A-1898598
; Sequence 1898598, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
```

```
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 1

RESULT 173
US-10-708-953A-1713144/c
; Sequence 1713144, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1713144
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1713144

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 1

RESULT 174
US-10-708-953A-1883139
; Sequence 1883139, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1883139
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1883139

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCGAGTTGAAGT 14
   |||||:::|
Db 1 GCCCAAGUUGCAGU 14

RESULT 175
US-10-708-953A-1898598
; Sequence 1898598, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
```

```
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1898598
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1898598

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCGCT 20
|:|||||:|:|:
Db 1 GUUGAAGGUGCCAU 14

RESULT 176
US-10-708-953A-2077386/c
; Sequence 2077386, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 05036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2077386
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2077386

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
|:|||||:|:|:
Db 14 CAGTGAAGTGCC 1

RESULT 177
US-10-709-572-163869/c
; Sequence 163869, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 163869
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-163869

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCG 19
|:|||||:|:|:

; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1898598
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1898598

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCGCT 20
|:|||||:|:|:
Db 1 GUUGAAGGUGCCAU 14

RESULT 178
US-10-709-572-191117/c
; Sequence 191117, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191117
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191117

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTT 15
|:|||||:|:|:
Db 14 CCCTGCTGAAGTT 1

RESULT 179
US-10-709-572-191263/c
; Sequence 191263, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191263
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191263

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCACGTTGAAGTTG 16
|:|||||:|:|:
Db 14 CCCTGCTGAAGTTG 1

RESULT 180
US-10-709-572-276392/c
; Sequence 276392, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
```


; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 276392
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-276392

Query Match 54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCCG 19
Db 14 AGTTGAAGTTGCTG 1

RESULT 181
PCT-US04-02720-1484/c
; Sequence 1484, Application PC/TUS0402720
; GENERAL INFORMATION:
; APPLICANT: Keck Graduate Institute
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Galas, David J.
; APPLICANT: Van Ness, Lori K.
; TITLE OF INVENTION: ORGANISM FINGERPRINTING USING NICKING
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 480188.422PC
; CURRENT APPLICATION NUMBER: PCT/US04/02720
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 1817
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1484
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amplification product
; NAME/KEY: misc_feature
; LOCATION: 7
; OTHER INFORMATION: n = A,T,C or G
PCT-US04-02720-1484

Query Match 50.0%; Score 10; DB 2; Length 13;
Score over Length 76.9%;
Best Local Similarity 90.9%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13
Db 13 CCCAGTNGAAG 3

RESULT 182
US-09-528-209A-6286
; Sequence 6286, Application US/09528209A
; GENERAL INFORMATION:
; APPLICANT: Agilent Technologies
; TITLE OF INVENTION: Computational Method for Constructing a Universal
; TITLE OF INVENTION: Tag-Antitag Molecular Array System for Hybridization
; TITLE OF INVENTION: Analysis
; FILE REFERENCE: 10992790
; CURRENT APPLICATION NUMBER: US/09/528,209A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 10286
; SOFTWARE: Bergefrom Sequence Formatter
; SEQ ID NO 6286
; LENGTH: 13
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A tag sequence incorporated in a probe nucleotide, the tag
; OTHER INFORMATION: sequence complementary to an antitag sequence incorporated
; OTHER INFORMATION: within a universal tag-antitag molecular array
US-09-528-209A-6286

Query Match 50.0%; Score 10; DB 24; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 4 GTTGAAGTTG 13

RESULT 183
US-10-051-645B-5965
; Sequence 5965, Application US/10051645B
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and
; TITLE OF INVENTION: Methods of use thereof for Diagnosis
; FILE REFERENCE: 1847.1009
; CURRENT APPLICATION NUMBER: US/10/051,645B
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 6908
; SEQ ID NO 5965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-051-645B-5965

Query Match 50.0%; Score 10; DB 38; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 3 GTTGAAGTTG 12

RESULT 184
US-10-257-017B-28743
; Sequence 28743, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 28743
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356
US-10-257-017B-28743

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 1 AGTTGAAGTT 10

RESULT 185

US-10-257-017B-28744/c
; Sequence 28744, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 28744
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356
US-10-257-017B-28744

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 13 AGTTGAAGTT 4

RESULT 186

US-10-257-017B-65609
; Sequence 65609, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 65609
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271
US-10-257-017B-65609

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 4 AGTTGAAGTT 13

RESULT 187

US-10-257-017B-65610/c

US-10-257-017B-65610/c
; Sequence 65610, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 65610
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271
US-10-257-017B-65610

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 10 AGTTGAAGTT 1

RESULT 188

US-10-257-017B-107775
; Sequence 107775, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107775
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982
US-10-257-017B-107775

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 3 AGTTGAAGTT 12

RESULT 189

US-10-257-017B-107776/c
; Sequence 107776, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107776
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982
US-10-257-017B-10776

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 15
DB      11 AGTTGAAGTT 2

RESULT 190
US-10-257-017B-131257
; Sequence 131257, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131257
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131257

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
DB      1 GTTGAAGTTG 10

RESULT 191
US-10-257-017B-131258/c
; Sequence 131258, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 131258
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131258

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
DB      13 GTTGAAGTTG 4

RESULT 192
US-10-257-017B-150111
; Sequence 150111, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150111
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150111

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      4 AGTTGAAGTT 13

RESULT 193
US-10-257-017B-150112/c
; Sequence 150112, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150112
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150112
```

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 10 AGTTGAAGTT 1

RESULT 194
US-10-257-017B-153411
; Sequence 153411, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 153411
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780
US-10-257-017B-153411

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 4e+06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
|||||
Db 2 AGTTGAAGATGY 13

RESULT 195
US-10-257-017B-153412/c
; Sequence 153412, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 153412
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780
US-10-257-017B-153412

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 4e+06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17

Db 12 AGTTGAAGATGY 1
|||||

RESULT 196
US-10-257-017B-171651
; Sequence 171651, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171651
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787
US-10-257-017B-171651

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 2 AGTTGAAGTT 11

RESULT 197
US-10-257-017B-171652/c
; Sequence 171652, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171652
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787
US-10-257-017B-171652

Query Match 50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 12 AGTTGAAGTT 3

RESULT 198
US-11-043-842-704
; Sequence 704, Application US/11043842

```

; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1004
; CURRENT APPLICATION NUMBER: US/11/043,842
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1028
; SEQ ID NO 704
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-11-043-842-704

Query Match      50.0%; Score 10; DB 62; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
      |||||
Db      3 GTTGAAGTTG 12

RESULT 199
US-11-051-720-809
; Sequence 809, Application US/11051720
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 809
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-11-051-720-809

Query Match      50.0%; Score 10; DB 62; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
      |||||
Db      3 GTTGAAGTTG 12

RESULT 200
US-11-711-827-704
; Sequence 704, Application US/11711827
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1004C
; CURRENT APPLICATION NUMBER: US/11/711,827
; CURRENT FILING DATE: 2007-02-28
; NUMBER OF SEQ ID NOS: 1028
; SEQ ID NO 704
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-11-711-827-704

; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1004
; CURRENT APPLICATION NUMBER: US/11/043,842
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1028
; SEQ ID NO 704
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-11-043-842-704

Query Match      50.0%; Score 10; DB 62; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
      |||||
Db      3 GTTGAAGTTG 12

RESULT 201
PCT-US02-25943-11543/c
; Sequence 11543, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 11543
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (1165178)...(1165192)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 12450
; PCT-US02-25943-11543

Query Match      57.0%; Score 11.4; DB 1; Length 15;
Score over Length 76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTGCCG 19
      |||||
Db      14 GTTGACGTTGCCG 2

RESULT 202
US-10-227-565-11543/c
; Sequence 11543, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 11543
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (1165178)...(1165192)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 12450
; US-10-227-565-11543

Query Match      57.0%; Score 11.4; DB 40; Length 15;
Score over Length 76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTGCCG 19
      |||||
Db      14 GTTGACGTTGCCG 2

RESULT 203
US-10-299-054A-10916
```

```
; Sequence 10916, Application US/10299054A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/299,054A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11910
; SOFTWARE: Proprietary
; SEQ ID NO 10916
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis complete genome.
; FEATURE:
; LOCATION: (3970758)...(3970772)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 13010
US-10-299-054A-10916

Query Match      57.0%; Score 11.4; DB 41; Length 15;
Score over Length 76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 1 GCCCCAGTTGAAG 13

RESULT 204
US-10-367-832A-11543/c
; Sequence 11543, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 11543
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (1165178)...(1165192)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 12450
US-10-367-832A-11543

Query Match      57.0%; Score 11.4; DB 46; Length 15;
Score over Length 76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
   ||||| |||||
Db 14 GTTGAAGTTGCCG 2

RESULT 205
US-10-708-953-383591
; Sequence 383591, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 383591
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-383591

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 206
US-10-708-953-409578
; Sequence 409578, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 409578
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-409578

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 207
US-10-708-953-572403
; Sequence 572403, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 572403
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-572403

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 3 GCCCCACUUGAAG 15
```

```
; ORGANISM: Homo sapiens
US-10-708-953-383591

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 206
US-10-708-953-409578
; Sequence 409578, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 409578
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-409578

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 207
US-10-708-953-572403
; Sequence 572403, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 572403
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-572403

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 208
US-10-708-953-716806
; Sequence 716806, Application US/10708953
; GENERAL INFORMATION:
```

```
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 716806
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-716806

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 209
US-10-708-953-1012891
; Sequence 1012891, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1012891
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1012891

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 210
US-10-708-953-1276947
; Sequence 1276947, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1276947
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1276947

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 211
US-10-708-953-1931848
; Sequence 1931848, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1931848
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1931848

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 212
US-10-708-953A-383591
; Sequence 383591, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 383591
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-383591

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 213
US-10-708-953A-409578
; Sequence 409578, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
```

..

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; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 409578
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-409578

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 214
US-10-708-953A-572403
; Sequence 572403, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 572403
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-572403

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 215
US-10-708-953A-716806
; Sequence 716806, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 716806
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-716806

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 216
US-10-708-953A-1012891
; Sequence 1012891, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1012891
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1012891

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 217
US-10-708-953A-1276947
; Sequence 1276947, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1276947
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1276947

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 218
US-10-708-953A-1931848
; Sequence 1931848, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1931848
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1931848

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15
```


US-10-708-953A-1931848

Query Match 57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13
| | | | | : | | | |
Db 3 GCCCAGTTGAAG 15

RESULT 219

US-10-708-952A-102785/c
; Sequence 102785, Application US/10708952A
; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A

; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 102785
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)

US-10-708-952A-102785

Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
| | | | | : | | | | |
Db 13 TTGATGTTGCCAT 1

RESULT 220

US-10-708-952A-105521/c
; Sequence 105521, Application US/10708952A
; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A

; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 105521
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)

US-10-708-952A-105521

Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18
| | | | | : | | | | |
Db 13 AATTGATGTTGCC 1

RESULT 221

US-10-708-952A-281446/c
; Sequence 281446, Application US/10708952A
; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 281446
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)

US-10-708-952A-281446

Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18
| | | | | : | | | | |
Db 13 AATTGATGTTGCC 1

RESULT 222

US-10-708-952A-283324/c
; Sequence 283324, Application US/10708952A
; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 283324
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)

US-10-708-952A-283324

Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
| | | | | : | | | | |
Db 13 TTGATGTTGCCAT 1

RESULT 223

US-10-708-952B-102785/c
; Sequence 102785, Application US/10708952B
; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 102785
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)

US-10-708-952B-102785

Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;

```
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGATGTTGCCAT 1
RESULT 224
US-10-708-952B-105521/c
; Sequence 105521, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 105521
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)
US-10-708-952B-105521
Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGCC 18
DB 13 AATTGATGTTGCC 1
RESULT 225
US-10-708-952B-281446/c
; Sequence 281446, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 281446
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)
US-10-708-952B-281446
Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGCC 18
DB 13 AATTGATGTTGCC 1
RESULT 226
US-10-708-952B-283324/c
; Sequence 283324, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
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; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 283324
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HAdV-B)
US-10-708-952B-283324
Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGATGTTGCCAT 1
RESULT 227
US-10-708-953-519962/c
; Sequence 519962, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 519962
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-519962
Query Match 49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGAAGATGCCAT 1
RESULT 228
US-10-708-953-683001/c
; Sequence 683001, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 683001
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-683001
Query Match 49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGAAGATGCCAT 1
RESULT 229
US-10-708-953-683001/c
; Sequence 683001, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 683001
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-683001
Query Match 49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
```

```
Db      ||||| ||||| |||||
      13 TTGAAGATGCCAT 1

RESULT 229
US-10-708-953-755878/c
; Sequence 755878, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 755878
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-755878

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
      ||||| ||||| |||||
Db      13 TTGAAGATGCCAT 1

RESULT 230
US-10-708-953-804357/c
; Sequence 804357, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 804357
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-804357

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
      ||||| ||||| |||||
Db      13 TTGAAGATGCCAT 1

RESULT 231
US-10-708-953-962280/c
; Sequence 962280, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 962280
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-962280

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCAGTTGAAGT 14
      ||||| ||||| |||||
Db      13 CCCAGTGCAAGT 1

RESULT 232
US-10-708-953-1014267
; Sequence 1014267, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1014267
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1014267

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
      ||||| ||||| |||||
Db      13 TTGAAGATGCCAT 1

RESULT 233
US-10-708-953-1125006/c
; Sequence 1125006, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1125006
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1125006

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
      ||||| ||||| |||||
Db      13 TTGAAGATGCCAT 1

RESULT 234
US-10-708-953-1151132/c
; Sequence 1151132, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1151132
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1151132/c

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
      ||||| ||||| |||||
Db      13 TTGAAGATGCCAT 1
```

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; Sequence 1151132, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1151132
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1151132

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 13 GTTCAAGTTGCTG 1

RESULT 235
US-10-708-953-1169509/c
; Sequence 1169509, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1169509
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1169509

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 13 GTTCAAGTTGCTG 1

RESULT 236
US-10-708-953-1571840/c
; Sequence 1571840, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1571840
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1571840

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAGT 14
Db 13 CCCAGTGCAAGT 1

RESULT 237
US-10-708-953-1618678/c
; Sequence 1618678, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1618678
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1618678

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
Db 13 TTGAAGATGCCAT 1

RESULT 238
US-10-708-953-1873083/c
; Sequence 1873083, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1873083
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1873083

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAGT 14
Db 13 CCCAGTGCAAGT 1

RESULT 239
US-10-708-953-2013164
; Sequence 2013164, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
```

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; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2013164
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2013164

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 53.8%; Pred. No. 5.1e+06;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
Db      1 UUGAAGGUGGUGU 13
      : : : : : : : : : : : : :
      : : : : : : : : : : : : :

RESULT 240
US-10-708-953-2083562/c
; Sequence 2083562, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2083562
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2083562

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTCAAGTTGCCG 19
Db      13 GTTCAAGTTGCTG 1
      : : : : : : : : : : : : :
      : : : : : : : : : : : : :

RESULT 241
US-10-708-953-2156300/c
; Sequence 2156300, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2156300
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2156300

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
Db      13 TTGAAGTTGCCAT 1
      : : : : : : : : : : : : :
      : : : : : : : : : : : : :

RESULT 242
US-10-708-953-2181596/c
; Sequence 2181596, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2181596
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2181596

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CCCAGTTCAAGTT 15
Db      13 CCCAGTTTCAGTT 1
      : : : : : : : : : : : : :
      : : : : : : : : : : : : :

RESULT 243
US-10-708-953A-519962/c
; Sequence 519962, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519962
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-519962

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
Db      13 TTGAAGTTGCCAT 1
      : : : : : : : : : : : : :
      : : : : : : : : : : : : :

RESULT 244
US-10-708-953A-683001/c
; Sequence 683001, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 683001
; LENGTH: 13
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-683001

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 245
US-10-708-953A-755878/c
; Sequence 755878, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 755878
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-755878

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 246
US-10-708-953A-804357/c
; Sequence 804357, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 804357
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-804357

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGT 14
   ||||| |||||
Db 13 CCCAGTGCAGT 1

RESULT 247
US-10-708-953A-962280/c
; Sequence 962280, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 962280
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-962280

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 248
US-10-708-953A-1014267
; Sequence 1014267, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1014267
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1014267

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 249
US-10-708-953A-1125006/c
; Sequence 1125006, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1125006
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1125006

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 1 UUGAAGGUGCUGU 13
```

Best Local Similarity 84.6%; Pred. No. 5.1e+06; Mismatches 0; Gaps 0; Indels 0;

QY 8 TTGAAGTTGCCGT 20
| | | | | | | |
Db 13 TTGAAGATGCCAT 1

RESULT 250

US-10-708-953A-1151132/c
; Sequence 1151132, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1151132
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1151132

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
| | | | | | | |
Db 13 GTTCAAGTTGCTG 1

RESULT 251

US-10-708-953A-1169509/c
; Sequence 1169509, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1169509
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1169509

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCAAGTTGAAGT 14
| | | | | | | |
Db 13 CCCCAAGTGAAGT 1

RESULT 252

US-10-708-953A-1571840/c
; Sequence 1571840, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A

; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1571840
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1571840

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTT 15
| | | | | | | |
Db 13 CCCAGTTTCAGTT 1

RESULT 253

US-10-708-953A-1618678/c
; Sequence 1618678, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1618678
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1618678

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCGT 20
| | | | | | | |
Db 13 TTGAAGATGCCAT 1

RESULT 254

US-10-708-953A-1873083/c
; Sequence 1873083, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1873083
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1873083

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCAAGTTGAAGT 14
| | | | | | | |
Db 13 CCCCAAGTGAAGT 1

```
; ORGANISM: Homo sapiens
US-10-708-953A-2156300

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
        ||||| |||||
Db      13 TTGAAGATGCCAT 1

RESULT 258
US-10-708-953A-2181596/c
; Sequence 2181596, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2181596
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2181596

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CCCAGTTGAAGTT 15
        ||||| |||||
Db      13 CCCAGTTTTCAGTT 1

RESULT 259
US-10-709-572-189555/c
; Sequence 189555, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189555
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-189555

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCAGTTGAAGT 14
        ||||| |||||
Db      13 CCCCTGCTGAAGT 1

RESULT 260
US-10-709-572-337591/c

; ORGANISM: Homo sapiens
US-10-708-953A-2013164

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 53.8%; Pred. No. 5.1e+06;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
        :|||: |||:
Db      1 UUGAAGGUGCUG 13

RESULT 256
US-10-708-953A-2083562/c
; Sequence 2083562, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2083562
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2083562

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCCG 19
        ||||| |||||
Db      13 GTTCAAGTTGCTG 1

RESULT 257
US-10-708-953A-2156300/c
; Sequence 2156300, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2156300
; LENGTH: 13
; TYPE: RNA
```


; Sequence 337591, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 337591
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-337591

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCC 18
|||||
DB 13 AGTTGAAGAGCC 1

RESULT 261

PCT-US06-29646A-101428/c
; Sequence 101428, Application PC/TUS0629646A
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, ELAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAS AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: PCT/US06/29646A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101428
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
PCT-US06-29646A-101428

Query Match 64.0%; Score 12.8; DB 3; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGC 17
|||||
DB 16 CCCAGGGGAAGTTGC 1

RESULT 262

US-10-535-164-454911/c
; Sequence 454911, Application US/10535164
; GENERAL INFORMATION:
; APPLICANT: BENTWICH, ITZHAK
; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and thereo
; FILE REFERENCE: 050992.0200.PCUS13
; CURRENT APPLICATION NUMBER: US/10/535,164
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 548156

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 454911
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Human
US-10-535-164-454911

Query Match 64.0%; Score 12.8; DB 48; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCC 18
|||||
DB 16 CCCAGGTGAAGTTGCC 1

RESULT 263

US-10-605-923-625220/c
; Sequence 625220, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 625220
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-625220

Query Match 64.0%; Score 12.8; DB 49; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCC 18
|||||
DB 16 CCCAGGTGAAGTTGCC 1

RESULT 264

US-10-707-975B-497939/c
; Sequence 497939, Application US/10707975B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Daniel, Kfar
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 06087.0201.CPUS01
; CURRENT APPLICATION NUMBER: US/10/707,975B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 664008
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 497939
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Human
US-10-707-975B-497939

Query Match 64.0%; Score 12.8; DB 51; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCC 18
|||||
DB 16 CCCAGGTGAAGTTGCC 1

```
RESULT 265
US-11-495-951A-101428/c
; Sequence 101428, Application US/11495951A
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 101428
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-101428

Query Match      64.0%; Score 12.8; DB 77; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAGTTGC 17
   ||||| |||||
Db 16 CCCAGGGGAAGTTGC 1

RESULT 266
US-10-708-953-1313224/c
; Sequence 1313224, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1313224
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1313224

Query Match      60.0%; Score 12; DB 52; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3

RESULT 267
US-10-708-953-1811627/c
; Sequence 1811627, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1811627

Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3

RESULT 268
US-10-708-953A-1313224/c
; Sequence 1313224, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1313224
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1313224

Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3

RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627

Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
Db 14 CCCAGTTGAAGT 3

RESULT 270
US-10-257-017B-272526
; Sequence 272526, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 272526
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonukleotid-Primer
US-10-257-017B-272526

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 4 AGTTGAAGT 12

RESULT 271
US-10-257-017B-281370/c
; Sequence 281370, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281370
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009690
US-10-257-017B-281370

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 11 GTTGAAGTT 3

RESULT 272
US-10-257-017B-284630/c
; Sequence 284630, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

```
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284630
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011911
US-10-257-017B-284630

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 12 AGTTGAAGT 4

RESULT 273
US-10-257-017B-288152
; Sequence 288152, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 288152
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013396
US-10-257-017B-288152

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10

RESULT 274
US-10-257-017B-298602
; Sequence 298602, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

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; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298602
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018187
US-10-257-017B-298602

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGAAGTTGC 17
Db 4 TGAAGTTGC 12

RESULT 275
US-10-257-017B-298745
; Sequence 298745, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298745
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020445
US-10-257-017B-298745

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 276
US-10-257-017B-299931
; Sequence 299931, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299931
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018813
US-10-257-017B-299931

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10

RESULT 277
US-10-257-017B-303341/c
; Sequence 303341, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303341
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020445
US-10-257-017B-303341

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 11 AGTTGAAGT 3

RESULT 278
US-10-257-017B-305026
; Sequence 305026, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305026
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021217
US-10-257-017B-305026

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
```

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Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 279
US-10-257-017B-307994
; Sequence 307994, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307994
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022828
US-10-257-017B-307994

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 280
US-10-257-017B-310012
; Sequence 310012, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310012
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023776
US-10-257-017B-310012

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10
```

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RESULT 281
US-10-257-017B-319646/c
; Sequence 319646, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 319646
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029341
US-10-257-017B-319646

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4

RESULT 282
US-10-257-017B-332564/c
; Sequence 332564, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 332564
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036994
US-10-257-017B-332564

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4

RESULT 283
US-10-257-017B-333972
; Sequence 333972, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

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; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 333972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037861
US-10-257-017B-333972

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTG 16
      |||||
Db      2 TTGAAGTTG 10

RESULT 284
US-10-257-017B-337673
; Sequence 337673, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337673
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039994
US-10-257-017B-337673

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTG 16
      |||||
Db      2 TTGAAGTTG 10

RESULT 285
US-10-257-017B-338530/c
; Sequence 338530, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338530
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005251
US-10-257-017B-338530

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTG 16
      |||||
Db      12 TTGAAGTTG 4

RESULT 286
US-10-257-017B-338626/c
; Sequence 338626, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338626
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040587
US-10-257-017B-338626

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTT 15
      |||||
Db      9 GTTGAAGTT 1

RESULT 287
US-10-257-017B-342781
; Sequence 342781, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 342781
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042707
US-10-257-017B-342781

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
| | | | | | | |
DB 1 TTGAAGTTG 9

RESULT 288
US-10-257-017B-343923/c
; Sequence 343923, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343923
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043299
US-10-257-017B-343923

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15
| | | | | | | |
DB 10 GTTGAAGTT 2

RESULT 289
US-10-257-017B-345821/c
; Sequence 345821, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 345821
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044228
US-10-257-017B-345821

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15
| | | | | | | |
DB 9 GTTGAAGTT 1

RESULT 290
US-10-257-017B-358109
; Sequence 358109, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358109
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050957
US-10-257-017B-358109

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
| | | | | | | |
DB 1 TTGAAGTTG 9

RESULT 291
US-10-257-017B-360215/c
; Sequence 360215, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 360215
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051979
US-10-257-017B-360215

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
| | | | | | | |
DB 10 AGTTGAAGT 2

RESULT 292

```
US-10-257-017B-365894/c
; Sequence 365894, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 365894
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055428
US-10-257-017B-365894

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGAAGTTG 16
Db      12 TTGAAGTTG 4

RESULT 293
US-10-257-017B-369254
; Sequence 369254, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369254
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057554
US-10-257-017B-369254

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GTTGAAGTT 15
Db      4 GTTGAAGTT 12

RESULT 294
US-10-257-017B-369635/c
; Sequence 369635, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
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; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369635
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057764
US-10-257-017B-369635

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGAAGTTG 16
Db      9 TTGAAGTTG 1

RESULT 295
US-10-257-017B-379943
; Sequence 379943, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379943
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063547
US-10-257-017B-379943

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGT 14
Db      4 AGTTGAAGT 12

RESULT 296
US-10-708-953-1574359/c
; Sequence 1574359, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1574359
; LENGTH: 12
; TYPE: RNA
```



```
; ORGANISM: Homo sapiens
US-10-708-953-1574359

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 297
US-10-708-953-1983714/c
; Sequence 1983714, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1983714
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1983714

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 298
US-10-708-953-2023470/c
; Sequence 2023470, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2023470
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2023470

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 299
US-10-708-953-2107113/c
; Sequence 2107113, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2107113
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2107113

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAA 12
   |||||
Db 10 CCAGTTGAA 2

RESULT 300
US-10-708-953A-1574359/c
; Sequence 1574359, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1574359
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1574359

Query Match      45.0%; Score 9; DB 53; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 301
US-10-708-953A-1983714/c
; Sequence 1983714, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1983714
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1983714

Query Match      45.0%; Score 9; DB 53; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAA 12
   |||||
Db 11 CCAGTTGAA 3

RESULT 299
US-10-708-953-2107113/c
; Sequence 2107113, Application US/10708953
; GENERAL INFORMATION:
```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGA 11
|||||
Db 12 CCAGTTGA 4

RESULT 302

US-10-708-953A-2023470/c
; Sequence 2023470, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2023470
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2023470

Query Match 45.0%; Score 9; DB 53; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAA 12
|||||
Db 11 CCAGTTGAA 3

RESULT 303

US-10-708-953A-2107113/c
; Sequence 2107113, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2107113
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2107113

Query Match 45.0%; Score 9; DB 53; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAA 12
|||||
Db 10 CCAGTTGAA 2

RESULT 304

US-09-168-519A-14/c
; Sequence 14, Application US/09168519A
; GENERAL INFORMATION:
; APPLICANT: Richelson, Elliott
; APPLICANT: Jansen, Karen
; TITLE OF INVENTION: Using Polyamide Nucleic Acid Oligomers
; TITLE OF INVENTION: to Engender a Biological Response
; FILE REFERENCE: 07039-107001
; CURRENT APPLICATION NUMBER: US/09/168,519A

; CURRENT FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-168-519A-14

Query Match 52.0%; Score 10.4; DB 20; Length 14;
Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
|||||
Db 14 CAGATGAAGTTG 3

RESULT 305

US-10-708-953-635436
; Sequence 635436, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 635436
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-635436

Query Match 52.0%; Score 10.4; DB 52; Length 14;
Score over Length 74.3%;
Best Local Similarity 75.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12
|||||
Db 3 GCUCCAGUUGAA 14

RESULT 306

US-10-708-953-842460
; Sequence 842460, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 842460
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-842460

Query Match 52.0%; Score 10.4; DB 52; Length 14;
Score over Length 74.3%;
Best Local Similarity 75.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12

```
Db      || |||||:||||
        3 GCUCGAGUUGAA 14

RESULT 307
US-10-708-953-1763210
; Sequence 1763210, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1763210
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1763210

Query Match      52.0%; Score 10.4; DB 52; Length 14;
Score over Length 74.3%;
Best Local Similarity 75.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAA 12
        || |||||:||||
Db      3 GCUCGAGUUGAA 14

RESULT 310
US-10-708-953A-1763210
; Sequence 1763210, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1763210
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1763210

Query Match      52.0%; Score 10.4; DB 53; Length 14;
Score over Length 74.3%;
Best Local Similarity 75.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAA 12
        || |||||:||||
Db      3 GCUCGAGUUGAA 14

RESULT 311
US-10-709-572-147851/C
; Sequence 147851, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 147851
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-147851

Query Match      52.0%; Score 10.4; DB 53; Length 14;
Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CAGTTGAAGTTG 16
        || |||||:||||
Db      14 CACTTGAAGTTG 3

RESULT 308
US-10-708-953A-635436
; Sequence 635436, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 635436
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-635436

Query Match      52.0%; Score 10.4; DB 53; Length 14;
Score over Length 74.3%;
Best Local Similarity 75.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAA 12
        || |||||:||||
Db      3 GCUCGAGUUGAA 14

RESULT 309
US-10-708-953A-842460
; Sequence 842460, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 842460
```

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RESULT 312
US-10-799-238-14/c
; SEQUENCE 14, Application US/10799238
; GENERAL INFORMATION:
; APPLICANT: Richelson, Elliott
; APPLICANT: Tyler, Beth Marie
; APPLICANT: Cusack, Bernadette Marie
; APPLICANT: Douglas, Christopher Lee
; APPLICANT: Jansen, Karen
; TITLE OF INVENTION: USING POLYAMIDE NUCLEIC ACID OLIGOMERS
; TITLE OF INVENTION: TO ENGENDER A BIOLOGICAL RESPONSE
; FILE REFERENCE: 07039/126001
; CURRENT APPLICATION NUMBER: US/10/799,238
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/168,791
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Rat
US-10-799-238-14
Query Match      52.0%; Score 10.4; DB 57; Length 14;
Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 14 CAGATGAAGTTG 3

RESULT 313
US-10-257-017B-61663
; SEQUENCE 61663, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 61663
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401
US-10-257-017B-61663
Query Match      48.0%; Score 9.6; DB 40; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17
Db 4 TTGAAGTTGY 13

RESULT 314
US-10-257-017B-61664/c
; SEQUENCE 61664, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 61664
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401
US-10-257-017B-61664
Query Match      48.0%; Score 9.6; DB 40; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17
Db 10 TTGAAGTTGY 1

RESULT 315
PCT-US02-25943-533
; SEQUENCE 533, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 533
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (50175)...(50190)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 574
PCT-US02-25943-533
Query Match      59.0%; Score 11.8; DB 1; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGC 17
Db 1 CCCAGTTGCAGGTGC 15

RESULT 316
US-09-708-690-5807
; SEQUENCE 5807, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
```

; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-708-690-5807

Query Match 59.0%; Score 11.8; DB 30; Length 16;
Score over Length 73.8%;
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
| | | | | : | | | | :
DB 2 GACCCAGAUGAAGUU 16

RESULT 317

US-09-870-161-5807
; Sequence 5807, Application US/09870161
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-M (400/026)
; CURRENT APPLICATION NUMBER: US/09/870.161
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 20821
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-870-161-5807

Query Match 59.0%; Score 11.8; DB 33; Length 16;
Score over Length 73.8%;
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
| | | | | : | | | | :
DB 2 GACCCAGAUGAAGUU 16

RESULT 318

US-10-227-565-533
; Sequence 533, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227.565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 533
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (50175)...(50190)

; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 574
US-10-227-565-533

Query Match 59.0%; Score 11.8; DB 40; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGC 17
| | | | | : | | | | :
DB 1 CCCAGTTGCAGGTGC 15

RESULT 319

US-10-287-949A-5807
; Sequence 5807, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287.949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5807

Query Match 59.0%; Score 11.8; DB 41; Length 16;
Score over Length 73.8%;
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
| | | | | : | | | | :
DB 2 GACCCAGAUGAAGUU 16

RESULT 320

US-10-287-949B-5807
; Sequence 5807, Application US/10287949B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 00-876-O (400/049)
; CURRENT APPLICATION NUMBER: US/10/287.949B
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949B-5807

Query Match 59.0%; Score 11.8; DB 41; Length 16;
Score over Length 73.8%;
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15

```
Db      2  GACCCAGGAAGUU 16
| | | | | : | | | | :
RESULT 321
US-10-287-949C-5807
; Sequence 5807, Application US/10287949C
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 00-876-O (400/053)
; CURRENT APPLICATION NUMBER: US/10/287,949C
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949C-5807

Query Match      59.0%; Score 11.8; DB 41; Length 16;
Score over Length 73.8%;
Best Local Similarity 66.7%; Pred. No. 5e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1  GCCCCAGTTGAAGTT 15
| | | | | : | | | | :
Db      2  GACCCAGGAAGUU 16
| | | | | : | | | | :
RESULT 322
US-10-367-832A-533
; Sequence 533, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 533
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (50175)...(50190)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 574
US-10-367-832A-533

Query Match      59.0%; Score 11.8; DB 46; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3  CCAAGTTGAAGTTGC 17
| | | | | : | | | | :
Db      1  CCAAGTTGAAGTTGC 15
| | | | | : | | | | :
RESULT 323
US-10-709-572-191130/c
; Sequence 191130, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
```

```
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191130
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191130

Query Match      59.0%; Score 11.8; DB 53; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2  CCCCAGTTGAAGTTG 16
| | | | | : | | | | :
Db      16  CCCCCTGCTGAAGTTG 2
| | | | | : | | | | :
RESULT 324
US-10-709-572-191264/c
; Sequence 191264, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191264
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191264

Query Match      59.0%; Score 11.8; DB 53; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2  CCCCAGTTGAAGTTG 16
| | | | | : | | | | :
Db      15  CCCCCTGCTGAAGTTG 1
| | | | | : | | | | :
RESULT 325
US-11-088-219-5807
; Sequence 5807, Application US/11088219
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, Dan
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; FILE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Fac
; FILE REFERENCE: MEHB00-876-O (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
```

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RESULT 329
US-10-714-333B-764639/c
; Sequence 764639, Application US/10714333B
; GENERAL INFORMATION:
; APPLICANT: Pharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfu
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333B
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333B-764639

Query Match 70.0%; Score 14; DB 55; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
|||||
Db 16 GTTGAAGTTGCCGT 3

RESULT 330

US-10-714-333C-764639/c
; Sequence 764639, Application US/10714333C
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10714,333C
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333C-764639

Query Match 70.0%; Score 14; DB 56; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
|||||
Db 16 GTTGAAGTTGCCGT 3

RESULT 331

US-11-083-784-764639/c
; Sequence 764639, Application US/11083784
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-764639

Query Match 70.0%; Score 14; DB 63; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
|||||
Db 16 GTTGAAGTTGCCGT 3

RESULT 332

US-11-093-832-764639/c
; Sequence 764639, Application US/11093832
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/093,832
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US/10714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-093-832-764639

Query Match 70.0%; Score 14; DB 64; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
|||||
Db 16 GTTGAAGTTGCCGT 3

RESULT 333

US-11-095-383-764639/c
; Sequence 764639, Application US/11095383
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30

; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-764639

Query Match 70.0%; Score 14; DB 65; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGCCGT 20
| | | | | | | | | | | | | | | | | | | | |
Db 16 GTTGAAGTTGCCGT 3

RESULT 334
US-11-101-244-764639/c
; Sequence 764639, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-764639

Query Match 70.0%; Score 14; DB 66; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGCCGT 20
| | | | | | | | | | | | | | | | | | | | |
Db 16 GTTGAAGTTGCCGT 3

RESULT 335
US-11-313-452-764639/c
; Sequence 764639, Application US/11313452
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/313,452

; CURRENT FILING DATE: 2005-12-21
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-313-452-764639

Query Match 70.0%; Score 14; DB 71; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGCCGT 20
| | | | | | | | | | | | | | | | | | | | |
Db 16 GTTGAAGTTGCCGT 3

RESULT 336
US-11-313-452A-764639/c
; Sequence 764639, Application US/11313452A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/313,452A
; CURRENT FILING DATE: 2005-12-21
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-313-452A-764639

Query Match 70.0%; Score 14; DB 72; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGCCGT 20
| | | | | | | | | | | | | | | | | | | | |
Db 16 GTTGAAGTTGCCGT 3

RESULT 337
US-10-299-054A-4597
; Sequence 4597, Application US/10299054A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/299,054A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11910
; SOFTWARE: Proprietary
; SEQ ID NO 4597
; LENGTH: 18
; TYPE: DNA

```
; ORGANISM: Mycobacterium tuberculosis complete genome.
; FEATURE:
; LOCATION: (1751704)...(1751721)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 5545
US-10-299-054A-4597

Query Match      66.0%; Score 13.2; DB 41; Length 18;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGCCG 19
   ||| ||||| |||||
Db 1 CCCAGTTGAAGAGCCG 18

RESULT 338
US-09-274-553-2617/c
; Sequence 2617, Application US/09274553A
; GENERAL INFORMATION:
; APPLICANT: RIBOZYME PHARMACEUTICALS, INC.
; APPLICANT: 2950 Wilderness Place
; APPLICANT: Boulder, Colorado 80301
; APPLICANT: USA
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS RELATED TO HEPATITIS C
; TITLE OF INVENTION: VIRUS INFECTION
; FILE REFERENCE: 241/078-PCT
; CURRENT APPLICATION NUMBER: US/09/274,553A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3118
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2617
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-274-553-2617

Query Match      55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
   ||| ||||| |||||
Db 15 CCCAGTTGAAG 5

RESULT 339
US-09-274-553B-1284/c
; Sequence 1284, Application US/09274553B
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553B
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
```

```
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553B-1284

Query Match      55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
   ||| ||||| |||||
Db 15 CCCAGTTGAAG 5

RESULT 340
US-09-274-553C-1284/c
; Sequence 1284, Application US/09274553C
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553C
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553C-1284

Query Match      55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
   ||| ||||| |||||
Db 15 CCCAGTTGAAG 5

RESULT 341
US-09-274-553D-1284/c
; Sequence 1284, Application US/09274553D
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
```

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; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1284

Query Match 55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 342
US-09-274-553E-1284/c
; Sequence 1284, Application US/09274553E
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553E
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553E-1284

Query Match 55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 343
US-09-504-231A-1284/c
; Sequence 1284, Application US/09504231A

```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-611-931A-1284

Query Match      55.0%; Score 11; DB 27; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAG 13
      |||||
Db      15 CCCAGTTGAAG 5

RESULT 345
US-09-611-931A-1284/c
; Sequence 1284, Application US/09611931
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: FDI 250/285
; CURRENT APPLICATION NUMBER: US/09/611,931
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-611-931A-1284

Query Match      55.0%; Score 11; DB 27; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAG 13
      |||||
Db      15 CCCAGTTGAAG 5

RESULT 346
US-09-611-931A-1284/c
; Sequence 1284, Application US/09611931A
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: MHB00-801-B (250/285)
; CURRENT APPLICATION NUMBER: US/09/611,931A
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-611-931A-1284

Query Match      55.0%; Score 11; DB 27; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAG 13
      |||||
Db      15 CCCAGTTGAAG 5

RESULT 347
US-09-708-690-4150/c
; Sequence 4150, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-708-690-4150

Query Match      55.0%; Score 11; DB 30; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CCAGTTGAAGT 14
      |||||
Db      15 CCAGTTGAAGT 5

RESULT 348
US-09-870-161-4150/c
; Sequence 4150, Application US/09870161
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MHB00-876-M (400/026)
; CURRENT APPLICATION NUMBER: US/09/870,161
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 20821
; SOFTWARE: PatentIn version 3.0
```

; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-870-161-4150

Query Match 55.0%; Score 11; DB 33; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
| | | | | | | | | |
DB 15 CCAGTTGAAGT 5

RESULT 349

US-10-287-949A-4150/c
; Sequence 4150, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4150

Query Match 55.0%; Score 11; DB 41; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
| | | | | | | | | |
DB 15 CCAGTTGAAGT 5

RESULT 350

US-10-287-949B-4150/c
; Sequence 4150, Application US/10287949B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-O (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949B
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949B-4150

Query Match 55.0%; Score 11; DB 41; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CCAGTTGAAGT 14
| | | | | | | | | |
DB 15 CCAGTTGAAGT 5

RESULT 351

US-10-287-949C-4150/c
; Sequence 4150, Application US/10287949C
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-O (400/053)
; CURRENT APPLICATION NUMBER: US/10/287,949C
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949C-4150

Query Match 55.0%; Score 11; DB 41; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
| | | | | | | | | |
DB 15 CCAGTTGAAGT 5

RESULT 352

US-10-951-303-4150/c
; Sequence 4150, Application US/10951303
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-4150

Query Match 55.0%; Score 11; DB 60; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 353
US-10-951-303B-4150/c
; Sequence 4150, Application US/10951303B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/158 (MBHB00-876-P)
; CURRENT APPLICATION NUMBER: US/10/951,303B
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8228
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-951-303B-4150

Query Match      55.0%; Score 11; DB 60; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 354
US-11-088-219-4150/c
; Sequence 4150, Application US/11088219
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Fac
; TITLE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBHB00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
```

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; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-4150

Query Match      55.0%; Score 11; DB 63; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 355
US-11-088-219A-4150/c
; Sequence 4150, Application US/11088219A
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/266 (MBHB00-876-Q)
; CURRENT APPLICATION NUMBER: US/11/088,219A
; CURRENT FILING DATE: 2005-03-23
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219A-4150

Query Match      55.0%; Score 11; DB 63; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 356
PCT-IL05-00263-27/c
; Sequence 27, Application PC/TIL0500263
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 29323
; CURRENT APPLICATION NUMBER: PCT/IL05/00263
; CURRENT FILING DATE: 2005-03-06
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
PCT-IL05-00263-27

Query Match      44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
```

```
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
   ||| ||| ||| |||
Db 12 CAGCTGAACCTG 1

RESULT 357
PCT-IL05-00263-29/c
; Sequence 29, Application PC/TIL0500263
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 29323
; CURRENT APPLICATION NUMBER: PCT/IL05/00263
; CURRENT FILING DATE: 2005-03-06
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
PCT-IL05-00263-29

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
   ||| ||| ||| |||
Db 12 CAGCTGAAGCTG 1

RESULT 358
PCT-IL05-00263-45/c
; Sequence 45, Application PC/TIL0500263
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 29323
; CURRENT APPLICATION NUMBER: PCT/IL05/00263
; CURRENT FILING DATE: 2005-03-06
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
PCT-IL05-00263-45

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
   ||| ||| ||| |||
Db 12 CAGTTGAACCTG 1

RESULT 359
PCT-US02-15103A-15
; Sequence 15, Application PC/TUS0215103A
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF MARYLAND, BALTIMORE
```

```
; APPLICANT: GONG, Da-Wei
; APPLICANT: SCHULDINER, Alan
; APPLICANT: YANG, Rongze
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: DG-2001-032
; CURRENT APPLICATION NUMBER: PCT/US02/15103A
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALT2 Exon 3, intron/exon junction, 3' splice acceptor
PCT-US02-15103A-15

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCAGTTGAAG 13
   ||| ||| ||| |||
Db 1 CCCCAGGTGATG 12

RESULT 360
PCT-US07-68401-1512
; Sequence 1512, Application PC/TUS0768401
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancowitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: PCT/US07/68401
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68401-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 6 AGTTGAAGTTGC 17
|||||
Db 1 AGTTGAATTC 12

RESULT 361
PCT-US07-68402-1512
; Sequence 1512, Application PC/TUS0768402
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF PTP1B
; FILE REFERENCE: CORE0061W015
; CURRENT APPLICATION NUMBER: PCT/US07/68402
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68402-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
|||||
Db 1 AGTTGAATTC 12

RESULT 362
PCT-US07-68403-1512
; Sequence 1512, Application PC/TUS0768403
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF APOB
; CURRENT APPLICATION NUMBER: PCT/US07/68403
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183

; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68403-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
|||||
Db 1 AGTTGAATTC 12

RESULT 363
PCT-US07-68404-1512
; Sequence 1512, Application PC/TUS0768404
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF PCSK9
; FILE REFERENCE: CORE0061W010
; CURRENT APPLICATION NUMBER: PCT/US07/68404
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68404-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17

Db 1 AGTTGAAATTC 12

RESULT 364

PCT-US07-68406-1512

Sequence 1512, Application PC/TUS0768406

GENERAL INFORMATION:

APPLICANT: Isis Pharmaceuticals, Inc.

APPLICANT: Sanjay Bhanot

APPLICANT: Richard S. Geary

APPLICANT: Robert McKay

APPLICANT: Brett P. Monia

APPLICANT: Punit P. Seth

APPLICANT: Andrew M. Siwkowski

APPLICANT: Eric E. Swayze

APPLICANT: Edward Wancewitz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

FILE REFERENCE: EXPRESSION OF SGLT2

CURRENT FILING DATE: 2007-05-25

PRIOR APPLICATION NUMBER: PCT/US07/68406

PRIOR FILING DATE: 2007-01-27

PRIOR APPLICATION NUMBER: 60/746,631

PRIOR FILING DATE: 2006-05-05

PRIOR APPLICATION NUMBER: 60/747,059

PRIOR FILING DATE: 2006-05-11

PRIOR APPLICATION NUMBER: 60/805,660

PRIOR FILING DATE: 2006-06-23

PRIOR APPLICATION NUMBER: 60/864,554

PRIOR FILING DATE: 2006-11-06

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1512

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

PCT-US07-68406-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 1.6e+07;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17

1 AGTTGAAATTC 12

RESULT 365

PCT-US07-68408-1512

Sequence 1512, Application PC/TUS0768408

GENERAL INFORMATION:

APPLICANT: Isis Pharmaceuticals, Inc.

APPLICANT: Sanjay Bhanot

APPLICANT: Richard S. Geary

APPLICANT: Robert McKay

APPLICANT: Brett P. Monia

APPLICANT: Punit P. Seth

APPLICANT: Andrew M. Siwkowski

APPLICANT: Eric E. Swayze

APPLICANT: Edward Wancewitz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

FILE REFERENCE: EXPRESSION OF CRP

CURRENT FILING DATE: 2007-05-25

PRIOR APPLICATION NUMBER: PCT/US07/68408

PRIOR FILING DATE: 2007-01-27

PRIOR APPLICATION NUMBER: 60/746,631

PRIOR FILING DATE: 2006-05-11

PRIOR APPLICATION NUMBER: 60/805,660

PRIOR FILING DATE: 2006-06-23

PRIOR APPLICATION NUMBER: 60/864,554

PRIOR FILING DATE: 2006-11-06

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1512

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

PCT-US07-68408-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 1.6e+07;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGC 17
1 AGTTGAAATTC 12
Db 1 AGTTGAAATTC 12
RESULT 366
PCT-US07-68410-1512
Sequence 1512, Application PC/TUS0768410
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Sanjay Bhanot
APPLICANT: Richard S. Geary
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Punit P. Seth
APPLICANT: Andrew M. Siwkowski
APPLICANT: Eric E. Swayze
APPLICANT: Edward Wancewitz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
FILE REFERENCE: EXPRESSION OF GCCR
CURRENT FILING DATE: 2007-05-25
PRIOR APPLICATION NUMBER: PCT/US07/68410
PRIOR FILING DATE: 2007-01-27
PRIOR APPLICATION NUMBER: 60/746,631
PRIOR FILING DATE: 2006-05-05
PRIOR APPLICATION NUMBER: 60/747,059
PRIOR FILING DATE: 2006-05-11
PRIOR APPLICATION NUMBER: 60/805,660
PRIOR FILING DATE: 2006-06-23
PRIOR APPLICATION NUMBER: 60/864,554
PRIOR FILING DATE: 2006-11-06
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1512
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68410-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGC 17
1 AGTTGAAATTC 12
Db 1 AGTTGAAATTC 12

RESULT 366
PCT-US07-68410-1512
Sequence 1512, Application PC/TUS0768410
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Sanjay Bhanot
APPLICANT: Richard S. Geary
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Punit P. Seth
APPLICANT: Andrew M. Siwkowski
APPLICANT: Eric E. Swayze
APPLICANT: Edward Wancewitz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
FILE REFERENCE: EXPRESSION OF GCCR
CURRENT FILING DATE: 2007-05-25
PRIOR APPLICATION NUMBER: PCT/US07/68410
PRIOR FILING DATE: 2007-01-27
PRIOR APPLICATION NUMBER: 60/746,631
PRIOR FILING DATE: 2006-05-05
PRIOR APPLICATION NUMBER: 60/747,059
PRIOR FILING DATE: 2006-05-11
PRIOR APPLICATION NUMBER: 60/805,660
PRIOR FILING DATE: 2006-06-23
PRIOR APPLICATION NUMBER: 60/864,554
PRIOR FILING DATE: 2006-11-06
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1512
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68410-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGC 17
1 AGTTGAAATTC 12
Db 1 AGTTGAAATTC 12

RESULT 367

PCT-US07-68412-1512
; Sequence 1512, Application PC/TUS0768412
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: EXPRESSION OF GCGR
; FILE REFERENCE: CORE0061W013
; CURRENT APPLICATION NUMBER: PCT/US07/68412
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68412-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAAGTTTC 12

RESULT 368

US-09-229-591-33
; Sequence 33, Application US/09229591
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR
; TITLE OF INVENTION: ANTAGONIST OBTAINED FROM A CDNA LIBRARY OF FETAL
; TITLE OF INVENTION: LIVER-SPLEEN
; FILE REFERENCE: 20411-743CON1
; CURRENT APPLICATION NUMBER: US/09/229,591
; CURRENT FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; EARLIER APPLICATION NUMBER: US 09/034,341
; EARLIER FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 33
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-229-591-33

Query Match 44.0%; Score 8.8; DB 21; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 1 CCACAGGTGAAG 12

RESULT 369

US-09-523-552-22
; Sequence 22, Application US/09523552
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36211
; CURRENT APPLICATION NUMBER: US/09/523,552
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: US 09/457,626
; EARLIER FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Exon
US-09-523-552-22

Query Match 44.0%; Score 8.8; DB 24; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 1 CCACAGGTGAAG 12

RESULT 370

US-10-004-382-22
; Sequence 22, Application US/10004382
; GENERAL INFORMATION:
; APPLICANT: Mize, Nancy K.

APPLICANT: Haley-Vicente, Dana A.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/36884A
CURRENT APPLICATION NUMBER: US/10/004,382
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/244,692
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Splice Acceptor Site
US-10-004-382-22

Query Match 44.0%; Score 8.8; DB 38; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCACAGTTGAAG 13
Db 1 CCACAGGTGAAG 12

RESULT 371

US-10-257-017B-275104/c
Sequence 275104, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 275104
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003785
US-10-257-017B-275104

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCACTTTAA 1

RESULT 372

US-10-257-017B-290891
Sequence 290891, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 290891
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014559
US-10-257-017B-290891

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGATGTAGC 12

RESULT 373

US-10-257-017B-317181/c
Sequence 317181, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 317181
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027856
US-10-257-017B-317181

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTGCCG 1

RESULT 374

US-10-257-017B-322885
Sequence 322885, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 322885
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031095
US-10-257-017B-322885

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
||| ||||| |||
Db 1 AGTAGAAGTGC 12

RESULT 375
US-10-257-017B-323132/c
; Sequence 323132, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323132
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031232
US-10-257-017B-323132

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAA 12
||| ||||| |||
Db 12 GCGCGAGTTGAA 1

RESULT 376
US-10-257-017B-326883
; Sequence 326883, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 326883
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033322
US-10-257-017B-326883

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
||| ||||| |||
Db 1 TGAGTTGTCT 12

RESULT 377
US-10-257-017B-327149/c
; Sequence 327149, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 327149
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033464
US-10-257-017B-327149

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
||| ||||| |||
Db 12 TGAAGTTGTCT 1

RESULT 378
US-10-257-017B-344782
; Sequence 344782, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344782
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043703
US-10-257-017B-344782

Query Match 44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
||| ||||| |||
Db 1 AGTTGAGATTGC 12

RESULT 379

```
US-10-257-017B-353467
; Sequence 353467, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353467
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048527
US-10-257-017B-353467
Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTGGCGT 20
Db 1 TGAAGTGGCGT 12

RESULT 380
US-10-257-017B-358049/c
; Sequence 358049, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358049
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050929
US-10-257-017B-358049
Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTGGCGT 20
Db 12 TGAAGTGGAGT 1

RESULT 381
US-10-257-017B-369872
; Sequence 369872, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

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; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369872
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057857
US-10-257-017B-369872
Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAAGTTGC 12

RESULT 382
US-10-257-017B-373811
; Sequence 373811, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 373811
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060333
US-10-257-017B-373811
Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAAGTTGC 12

RESULT 383
US-10-477-086-15
; Sequence 15, Application US/10477086
; GENERAL INFORMATION:
; APPLICANT: GONG, De-Wei
; APPLICANT: SCHULDNER, Alan
; APPLICANT: YANG, Rongze
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: UMB-01-032
; CURRENT APPLICATION NUMBER: US/10/477,086
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: PCT/US02/15103
; PRIOR FILING DATE: 2002-05-14
```

```
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALt2 Exon 3, intron/exon junction, 3' splice acceptor
US-10-477-086-15

Query Match      44.0%; Score 8.8; DB 47; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTCGAAG 13
Db 1 CCCAGGTGATG 12

RESULT 384
US-10-591-442-27/c
; Sequence 27, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-27

Query Match      44.0%; Score 8.8; DB 48; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGTTG 1

RESULT 385
US-10-591-442-29/c
; Sequence 29, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-29

Query Match      44.0%; Score 8.8; DB 48; Length 12;
```

```
; Score over Length 73.3%;
; Best Local Similarity 83.3%; Pred. No. 1.6e+07;
; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 386
US-10-591-442-45/c
; Sequence 45, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-45

Query Match      44.0%; Score 8.8; DB 48; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGTTGAACCTG 1

RESULT 387
US-10-708-952A-111659/c
; Sequence 111659, Application US/10708952A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111659
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Human adenovirus E
; OTHER INFORMATION:
US-10-708-952A-111659

Query Match      44.0%; Score 8.8; DB 51; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
Db 12 TGAGTTGCTGT 1

RESULT 388
US-10-708-952A-289071/c
; Sequence 289071, Application US/10708952A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
```

; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF

; FILE REFERENCE: 55035

; CURRENT APPLICATION NUMBER: US/10/708,952A

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 399737

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 289071

; LENGTH: 12

; TYPE: RNA

; ORGANISM: Human adenovirus E

US-10-708-952A-289071

Query Match 44.0%; Score 8.8; DB 51; Length 12;

Score over Length

Best Local Similarity 83.3%; Pred. No. 1.6e+07;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20

||| ||||| |||

Db 12 TGAGGTTGCTGT 1

RESULT 389

US-10-708-952B-111659/c

; Sequence 111659, Application US/10708952B

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; APPLICANT: Bentwich, Itzhak

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL

; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF

; FILE REFERENCE: 06087.0301.CPUS00

; CURRENT APPLICATION NUMBER: US/10/708,952B

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 399738

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 111659

; LENGTH: 12

; TYPE: RNA

; ORGANISM: Human adenovirus E

US-10-708-952B-111659

Query Match 44.0%; Score 8.8; DB 51; Length 12;

Score over Length

Best Local Similarity 83.3%; Pred. No. 1.6e+07;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20

||| ||||| |||

Db 12 TGAGGTTGCTGT 1

RESULT 390

US-10-708-952B-289071/c

; Sequence 289071, Application US/10708952B

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; APPLICANT: Bentwich, Itzhak

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL

; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF

; FILE REFERENCE: 06087.0301.CPUS00

; CURRENT APPLICATION NUMBER: US/10/708,952B

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 399738

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 289071

; LENGTH: 12

; TYPE: RNA

; ORGANISM: Human adenovirus E

US-10-708-952B-289071

Query Match 44.0%; Score 8.8; DB 51; Length 12;

Score over Length

Best Local Similarity 83.3%; Pred. No. 1.6e+07;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20

||| ||||| |||

Db 12 TGAGGTTGCTGT 1

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20

||| ||||| |||

Db 12 TGAGGTTGCTGT 1

RESULT 391

US-10-708-953-391440

; Sequence 391440, Application US/10708953

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY

; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF

; FILE REFERENCE: 55036

; CURRENT APPLICATION NUMBER: US/10/708,953

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 2254510

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 391440

; LENGTH: 12

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-708-953-391440

Query Match 44.0%; Score 8.8; DB 52; Length 12;

Score over Length

Best Local Similarity 58.3%; Pred. No. 1.6e+07;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15

||| :||| :

Db 1 CCUGUUGAAGCU 12

RESULT 392

US-10-708-953-426502/c

; Sequence 426502, Application US/10708953

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY

; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF

; FILE REFERENCE: 55036

; CURRENT APPLICATION NUMBER: US/10/708,953

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 2254510

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 426502

; LENGTH: 12

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-708-953-426502

Query Match 44.0%; Score 8.8; DB 52; Length 12;

Score over Length

Best Local Similarity 83.3%; Pred. No. 1.6e+07;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20

||| ||||| |||

Db 12 TGCAGTGGCCGT 1

RESULT 393

US-10-708-953-448734/c

; Sequence 448734, Application US/10708953

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY

; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF

; FILE REFERENCE: 55036

; CURRENT APPLICATION NUMBER: US/10/708,953

; CURRENT FILING DATE: 2004-04-02

```
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448734
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-448734

Query Match          44.0%; Score 8.8; DB 52; Length 12;
Score over Length    73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTTCAG 1

RESULT 394
US-10-708-953-451057/c
; Sequence 451057, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 451057
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-451057

Query Match          44.0%; Score 8.8; DB 52; Length 12;
Score over Length    73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 395
US-10-708-953-467798/c
; Sequence 467798, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 467798
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-467798

Query Match          44.0%; Score 8.8; DB 52; Length 12;
Score over Length    73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 396
US-10-708-953-467798/c
; Sequence 467798, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 467798
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-467798

Query Match          44.0%; Score 8.8; DB 52; Length 12;
Score over Length    73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 397
US-10-708-953-580776
; Sequence 580776, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580776
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-580776

Query Match          44.0%; Score 8.8; DB 52; Length 12;
Score over Length    73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1

RESULT 398
US-10-708-953-580776
; Sequence 580776, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580776
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-580776

Query Match          44.0%; Score 8.8; DB 52; Length 12;
Score over Length    73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1

RESULT 399
US-10-708-953-580776
; Sequence 580776, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580776
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-580776

Query Match          44.0%; Score 8.8; DB 52; Length 12;
Score over Length    73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1
```


US-10-708-953-752554

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAA 12
||| ||| :|||
DB 1 GCCUCAUUGAA 12

RESULT 399

US-10-708-953-770756
; Sequence 770756, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 770756
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-770756

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTT 15
||| :||| :
DB 1 CCUGUGAAGCU 12

RESULT 400

US-10-708-953-787100/c
; Sequence 787100, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 787100
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-787100

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAA 12
||| ||| :|||
DB 12 GCCCCTGATGAA 1

RESULT 401

US-10-708-953-863477/c
; Sequence 863477, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 863477
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-863477

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
||| ||| |||
DB 12 TGCAGTGGCGT 1

RESULT 402

US-10-708-953-924430/c
; Sequence 924430, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 924430
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-924430

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
||| ||| |||
DB 12 TTGAAGTTTCAG 1

RESULT 403

US-10-708-953-925708/c
; Sequence 925708, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 925708
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-925708

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 9 TGAAGTTGCCGT 20
Db 12 TCAGTGGCCGT 1

RESULT 404
US-10-708-953-958234/c
; Sequence 958234, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 958234
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-958234
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAACCC 1

RESULT 405
US-10-708-953-1033680/c
; Sequence 1033680, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1033680
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1033680
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAACCC 1

RESULT 406
US-10-708-953-1041658
; Sequence 1041658, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1041658
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1041658
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1

RESULT 407
US-10-708-953-1316830/c
; Sequence 1316830, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1316830
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1316830
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13
Db 12 CCCAGGTAAG 1

RESULT 408
US-10-708-953-1342582
; Sequence 1342582, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1342582
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1342582
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 1 CAUUUGAACUUG 12

RESULT 409
US-10-708-953-1342582
; Sequence 1342582, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1342582
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1342582
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 409

US-10-708-953-1378924
; Sequence 1378924, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1378924
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1378924

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTT 15
|||:|||||:
Db 1 CCUGUGAAGCU 12

RESULT 410

US-10-708-953-1380444/c
; Sequence 1380444, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1380444
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1380444

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
|||||||:
Db 12 TTGAAGTTTCAG 1

RESULT 411

US-10-708-953-1539333/c
; Sequence 1539333, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1539333
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1539333

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
|||:|||||:
Db 12 TGCAGTGGCCGT 1

RESULT 412

US-10-708-953-1669231/c
; Sequence 1669231, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1669231
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1669231

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
|||||||:
Db 12 GTTGAAGAAGCC 1

RESULT 413

US-10-708-953-1754748/c
; Sequence 1754748, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1754748
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1754748

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
|||:|||||:
Db 12 CTGCTGAAGTTG 1

RESULT 414

US-10-708-953-1858055
; Sequence 1858055, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY

; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1858055
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1858055

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15
Db 1 CCUGUUGAACU 12

RESULT 415
US-10-708-953-1868045/c
; Sequence 1868045, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1868045
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1868045

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1

RESULT 416
US-10-708-953-1886720
; Sequence 1886720, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1886720
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1886720

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 50.0%; Pred. No. 1.6e+07;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
Db 1 CAUUGAACUUG 12

RESULT 417
US-10-708-953-2003791
; Sequence 2003791, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2003791
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2003791

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 1 GCCUCAUUGAA 12

RESULT 418
US-10-708-953-2054387/c
; Sequence 2054387, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2054387
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2054387

Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGCAGTGCCGT 1

RESULT 419
US-10-708-953-2142733/c
; Sequence 2142733, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 2142733
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2142733

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 12 CCCAGGTAAG 1

RESULT 420
US-10-708-953-2179457/c
; Sequence 2179457, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2179457
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2179457

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 421
US-10-708-953-2206794/c
; Sequence 2206794, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2206794
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2206794

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTTCAG 1

RESULT 422
US-10-708-953-2206794/c
; Sequence 2206794, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2206794
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2206794

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGCAGTGGCCGT 1

RESULT 424
US-10-708-953A-448734/c
; Sequence 448734, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 448734
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-448734

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15
Db 1 CCUGUUGAAGCU 12

RESULT 423
US-10-708-953A-426502/c
; Sequence 426502, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426502
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-426502

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15
Db 1 CCUGUUGAAGCU 12

RESULT 423
US-10-708-953A-426502/c
; Sequence 426502, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426502
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-426502

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGCAGTGGCCGT 1

RESULT 424
US-10-708-953A-448734/c
; Sequence 448734, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 448734
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-448734
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Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTTCAG 1

RESULT 425
US-10-708-953A-451057/c
; Sequence 451057, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 451057
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-451057

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 426
US-10-708-953A-467798/c
; Sequence 467798, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467798
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-467798

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 427
US-10-708-953A-524180/c
; Sequence 524180, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
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; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 524180
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-524180

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1

RESULT 428
US-10-708-953A-580776
; Sequence 580776, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 580776
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-580776

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 1 GCCUCAUUGAA 12

RESULT 429
US-10-708-953A-752554
; Sequence 752554, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 752554
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-752554

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
```

```
Db      1  GCCUCAUUUGAA 12
|||||  |||  |||  |||  |||
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-863477

RESULT 430
US-10-708-953A-770756
; Sequence 770756, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 770756
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-770756

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CCAGTTGAAGTT 15
|||||  |||  |||  |||  |||
Db      1  CCUGUUGAAGCU 12

RESULT 431
US-10-708-953A-787100/c
; Sequence 787100, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 787100
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-787100

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CCAGTTGAAGTT 15
|||||  |||  |||  |||  |||
Db      1  CCUGUUGAAGCU 12

RESULT 432
US-10-708-953A-863477/c
; Sequence 863477, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 863477

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAA 12
|||||  |||  |||  |||  |||
Db      12  GCCCCAGTTGAA 1

RESULT 433
US-10-708-953A-924430/c
; Sequence 924430, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 924430
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-924430

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8  TTGAAGTTGCCG 19
|||||  |||  |||  |||  |||
Db      12  TTGAAGTTTCAG 1

RESULT 434
US-10-708-953A-925708/c
; Sequence 925708, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 925708
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-925708

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9  TGAAGTTGCCGT 20
|||||  |||  |||  |||  |||
Db      12  TGAAGTTGCCGT 1

RESULT 435
US-10-708-953A-958234/c
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; Sequence 958234, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 958234
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-958234

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGAAGAGGCC 1

RESULT 436
US-10-708-953A-1033680/c
; Sequence 1033680, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1033680
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1033680

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCCCAGTTGAA 12
Db      12 GCCCCTGATGAA 1

RESULT 437
US-10-708-953A-1041658
; Sequence 1041658, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1041658
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1041658

Query Match      44.0%; Score 8.8; DB 53; Length 12;
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Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CCACTTGAAGTT 15
Db      1 CCUGUGAAGCU 12

RESULT 438
US-10-708-953A-1316830/c
; Sequence 1316830, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1316830
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1316830

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCAGTTGAAG 13
Db      12 CCCAGGTAAAG 1

RESULT 439
US-10-708-953A-1342582
; Sequence 1342582, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1342582
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1342582

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 50.0%; Pred. No. 1.6e+07;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      5 CAGTTGAAGTTG 16
Db      1 CAUUGAAGCUG 12

RESULT 440
US-10-708-953A-1378924
; Sequence 1378924, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
```



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; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1378924
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1378924

Query Match 44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTT 15
DB 1 CCUGUUGAGCU 12

RESULT 441
US-10-708-953A-1380444/c
; Sequence 1380444, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1380444
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1380444

Query Match 44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
DB 12 TTGAAGTTTCAG 1

RESULT 442
US-10-708-953A-1539333/c
; Sequence 1539333, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1539333
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1539333

Query Match 44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 12 TGAAGTTGCCGT 20

; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1378924
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1378924

Query Match 44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTT 15
DB 1 CCUGUUGAGCU 12

RESULT 441
US-10-708-953A-1380444/c
; Sequence 1380444, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1380444
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1380444

Query Match 44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
DB 12 TTGAAGTTTCAG 1

RESULT 442
US-10-708-953A-1539333/c
; Sequence 1539333, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1539333
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1539333

Query Match 44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 12 TGAAGTTGCCGT 20

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1858055

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15
   |||:::|||||:
Db 1 CCUGUGAAGCU 12

RESULT 446
US-10-708-953A-1868045/c
; Sequence 1868045, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1868045
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1868045

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
   |||||:||||
Db 12 GCCCCTGATGA 1

RESULT 447
US-10-708-953A-1886720
; Sequence 1886720, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1886720
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1886720

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 50.0%; Pred. No. 1.6e+07;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
   |||:::|||||:
Db 1 CAUUGAACUUG 12

RESULT 448
US-10-708-953A-2003791
; Sequence 2003791, Application US/10708953A

; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2003791
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2003791

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
   |||||:||||
Db 1 GCCUCAUUGAA 12

RESULT 449
US-10-708-953A-2054387/c
; Sequence 2054387, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2054387
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2054387

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
   |||||:|||||
Db 12 TGCAGTGGCCGT 1

RESULT 450
US-10-708-953A-2142733/c
; Sequence 2142733, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2142733
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2142733

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
```

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; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190034
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-190034

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 12 CCCAGTTGAAG 1

RESULT 451
US-10-708-953A-2179457/c
; Sequence 2179457, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2179457
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2179457

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAGCC 1

RESULT 452
US-10-708-953A-2206794/c
; Sequence 2206794, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2206794
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2206794

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTGAG 1

RESULT 453
US-10-709-572-190034/c
; Sequence 190034, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
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; ;

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; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190034
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-190034

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 12 CCCCTGCTGAAG 1

RESULT 454
US-10-709-572-225526/c
; Sequence 225526, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 225526
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-225526

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAAGCTGCTGT 1

RESULT 455
US-10-709-572-258617
; Sequence 258617, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 258617
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-258617

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
```

Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAA 12
||| ||| ||| |||
Db 1 GCTCCAGTGGAA 12

RESULT 456
US-10-709-572-260004/c
; Sequence 260004, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amiel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 260004
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-260004

Query Match 44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
||||| ||| |||
Db 12 TTGAAGTTGCAG 1

RESULT 457
US-11-126-421-15
; Sequence 15, Application US/11126421
; GENERAL INFORMATION:
; APPLICANT: GONG, Da-Wei
; APPLICANT: SCHULDNER, Alan
; APPLICANT: YANG, Rongze
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: UMB-01-032
; CURRENT APPLICATION NUMBER: US/11/126,421
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/10/477,086
; PRIOR FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: PCT/US02/15103
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALT2 Exon 3, intron/exon junction, 3' splice acceptor
US-11-126-421-15

Query Match 44.0%; Score 8.8; DB 66; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13

Db 1 CCCAGGTGATG 12
||||| ||| |

RESULT 458
US-11-438-135-357
; Sequence 357, Application US/11438135
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Gingeras, Thomas R.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Garrett Miyada, Charles
; APPLICANT: Morris, Macdonald S.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 585
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: 2 Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/438,135
; FILING DATE: 19-MAY-2006
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,521
; FILING DATE: 02-Aug-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 357:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-11-438-135-357

Query Match 44.0%; Score 8.8; DB 75; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
||||| ||| |||
Db 1 TGGAGTTGCAGT 12

RESULT 459
US-11-438-135-358
; Sequence 358, Application US/11438135
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Ginetas, Thomas R.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 585
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: 2 Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/438,135
; FILING DATE: 19-MAY-2006
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,521
; FILING DATE: 02-Aug-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-11-438-135-358

Query Match 44.0%; Score 8.8; DB 75; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTTGC 17
Db 1 ATTTGAGTTGC 12

RESULT 460
US-11-585-939A-7/c

; Sequence 7, Application US/11585939A
; GENERAL INFORMATION:
; APPLICANT: HAYASHI, Miho
; APPLICANT: MORI, Kazuyoshi
; APPLICANT: MAEDA, Mizuo
; TITLE OF INVENTION: DNA SEPARATION DEVICE, DNA SEPARATION METHOD, AND LIGAND DNA
; FILE REFERENCE: 2006_1856A
; CURRENT APPLICATION NUMBER: US/11/585,939A
; CURRENT FILING DATE: 2006-10-25
; PRIOR APPLICATION NUMBER: JP 2005-311933
; PRIOR FILING DATE: 2005-10-26
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-585-939A-7
Query Match 44.0%; Score 8.8; DB 78; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CCCAGTTGAAG 13
Db 12 CCCAGCGCAAG 1
RESULT 461
US-11-745-429-1512
; Sequence 1512, Application US/11745429
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancowitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: GENE EXPRESSION
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: US/11/745,429
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-11-745-429-1512
Query Match 44.0%; Score 8.8; DB 81; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAATTC 12

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; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Splice Acceptor Site
US-60-244-692-22

Query Match 44.0%; Score 8.8; DB 87; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 1 CCACAGTGAAG 12

RESULT 464
US-09-546-745A-4860/C
; Sequence 4860, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4860
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-4860

Query Match 62.0%; Score 12.4; DB 25; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGC 17
Db 16 CCAGTTGAAGCTGC 3

RESULT 465
US-09-546-745A-4861/C
; Sequence 4861, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A

```

```
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4861
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-4861

Query Match      62.0%; Score 12.4; DB 25; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGC 17
Db 15 CCAGTTGAAGTTGC 2

RESULT 466
US-10-605-923-508977
; Sequence 508977, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 508977
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-508977

Query Match      62.0%; Score 12.4; DB 49; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGTTG 16
Db 1 CCCAGTTGAAGATG 14

RESULT 467
PCT-US05-37925-39/c
; Sequence 39, Application PC/TUS0537925
; GENERAL INFORMATION:
; APPLICANT: Hitachi Chemical Co., Ltd.
; APPLICANT: Hitachi Chemical Research Center, Inc
; APPLICANT: MITSUHASHI, Masato
; TITLE OF INVENTION: METHOD FOR TAILORING ADMINISTRATION OF
; TITLE OF INVENTION: DRUGS BY QUANTITATION OF MRNA
; FILE REFERENCE: HITACHI.066VPC
; CURRENT APPLICATION NUMBER: PCT/US05/37925
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/620,603
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/653,557
; PRIOR FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: 60/688,741
; PRIOR FILING DATE: 2005-06-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence

Query Match      80.0%; Score 16; DB 3; Length 22;
Score over Length 72.7%;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 468
PCT-US05-37925-51/c
; Sequence 51, Application PC/TUS0537925
; GENERAL INFORMATION:
; APPLICANT: Hitachi Chemical Co., Ltd.
; APPLICANT: Hitachi Chemical Research Center, Inc
; APPLICANT: MITSUHASHI, Masato
; TITLE OF INVENTION: METHOD FOR TAILORING ADMINISTRATION OF
; TITLE OF INVENTION: DRUGS BY QUANTITATION OF MRNA
; FILE REFERENCE: HITACHI.066VPC
; CURRENT APPLICATION NUMBER: PCT/US05/37925
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/620,603
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/653,557
; PRIOR FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: 60/688,741
; PRIOR FILING DATE: 2005-06-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer sequence
PCT-US05-37925-51

Query Match      80.0%; Score 16; DB 3; Length 22;
Score over Length 72.7%;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 469
PCT-US06-00086-6/c
; Sequence 6, Application PC/TUS0600086
; GENERAL INFORMATION:
; APPLICANT: Murakami, Taku
; TITLE OF INVENTION: PRIMER GENERATION ROLLING CIRCLE
; TITLE OF INVENTION: AMPLIFICATION
; FILE REFERENCE: HITACHI.067VPC
; CURRENT APPLICATION NUMBER: PCT/US06/00086
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US 60/641,255
; PRIOR FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically prepared oligonucleotide sequence
PCT-US06-00086-6
```

```
Query Match      80.0%; Score 16; DB 3; Length 22;
Score over Length 72.7%;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
   |||||
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 470
US-10-605-923-810848
; Sequence 810848, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 810848
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-810848

Query Match      69.0%; Score 13.8; DB 49; Length 19;
Score over Length 72.6%;
Best Local Similarity 88.2%; Pred. No. 4.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGCC 18
   |||
Db 3 CCACATTTGAAGTTGCC 19

RESULT 471
US-10-605-924-801404/c
; Sequence 801404, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 801404
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-801404

Query Match      69.0%; Score 13.8; DB 50; Length 19;
Score over Length 72.6%;
Best Local Similarity 88.2%; Pred. No. 4.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGCC 18
   |||
Db 17 CCACATTTGAAGTTGCC 1

RESULT 472
US-09-528-209A-6207
; Sequence 6207, Application US/09528209A
; GENERAL INFORMATION:
; APPLICANT: Agilent Technologies
; TITLE OF INVENTION: Computational Method for Constructing a Universal
```

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; TITLE OF INVENTION: Tag-Antitag Molecular Array System for Hybridization
; FILE REFERENCE: 10992790
; CURRENT APPLICATION NUMBER: US/09/528,209A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 10286
; SOFTWARE: Bergstrom Sequence Formatter
; SEQ ID NO 6207
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A tag sequence incorporated in a probe nucleotide, the tag
; OTHER INFORMATION: sequence complementary to an antitag sequence incorporated
; OTHER INFORMATION: within a universal tag-antitag molecular array
US-09-528-209A-6207

Query Match      47.0%; Score 9.4; DB 24; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 3 AGTTGAAGTTG 13

RESULT 473
US-10-257-017B-6223
; Sequence 6223, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 6223
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001948
US-10-257-017B-6223

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 3 AGTTGAAGTTG 13

RESULT 474
US-10-257-017B-6224/c
; Sequence 6224, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```



```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 6224
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001948
US-10-257-017B-6224

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      11 AGTAGAAGTTG 1

RESULT 475
US-10-257-017B-12629
; Sequence 12629, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12629
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12629

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      2 AGTTGATGTTG 12

RESULT 476
US-10-257-017B-12630/c
; Sequence 12630, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12630/c

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      2 AGTTGATGTTG 12

RESULT 477
US-10-257-017B-25055
; Sequence 25055, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25055
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25055

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 TGAAGTTGCCG 19
Db      3 TGAAGTTGCCG 13

RESULT 478
US-10-257-017B-25056/c
; Sequence 25056, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25056
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25056

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 9 TGAAGTTCCG 19
Db 11 TGAAGTTGCG 1

RESULT 479
US-10-257-017B-25081
; Sequence 25081, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25081
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006096
US-10-257-017B-25081

Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.le+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 2 AGTGAAGTTG 12

RESULT 480
US-10-257-017B-25082/c
; Sequence 25082, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25082
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006096
US-10-257-017B-25082

Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.le+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 12 AGTGAAGTTG 2

RESULT 481

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US-10-017B-27969
; Sequence 27969, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27969
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007879
US-10-017B-27969

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      1 AGTTGAAGTTG 11

RESULT 482
US-10-017B-27970/c
; Sequence 27970, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27970
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007879
US-10-017B-27970

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 483
US-10-017B-36537
; Sequence 36537, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

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; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 36537
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36537

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 ATTGAAGTTG 11

RESULT 484
US-10-257-017B-36538/c
; Sequence 36538, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 36538
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36538

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 ATTGAAGTTG 3

RESULT 485
US-10-257-017B-56753
; Sequence 56753, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

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; SEQ ID NO 56753
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56753

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAATTTG 11

RESULT 486
US-10-257-017B-56754/c
; Sequence 56754, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 56754
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56754

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAATTTG 3

RESULT 487
US-10-257-017B-96965
; Sequence 96965, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96965
```

Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
|||||
DB 1 TGAAGTTGCCG 11

RESULT 488
US-10-257-017B-96966/c
; Sequence 96966, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96966
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96966

Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
|||||
DB 13 TGAAGTTGCCG 3

RESULT 489
US-10-257-017B-111321
; Sequence 111321, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111321
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111321

Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16

Db 3 AGTTGATGTTG 13
|||||

RESULT 490
US-10-257-017B-111322/c
; Sequence 111322, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111322
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111322

Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
DB 11 AGTTGATGTTG 1

RESULT 491
US-10-257-017B-117287
; Sequence 117287, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117287
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345
US-10-257-017B-117287

Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
DB 3 AGTTGATGTTG 13

RESULT 492
US-10-257-017B-117288/c
; Sequence 117288, Application US/10257017B

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117288
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345
US-10-257-017B-117288

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      11 AGTTGTAAGTTG 1

RESULT 493
US-10-257-017B-117509
; Sequence 117509, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117509
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385
US-10-257-017B-117509

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      3 AGTTGAAATTG 13

RESULT 494
US-10-257-017B-117510/c
; Sequence 117510, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
```

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; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117510
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385
US-10-257-017B-117510

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      11 AGTTGAAATTG 1

RESULT 495
US-10-257-017B-187027
; Sequence 187027, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187027
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187027

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      1 AGTTGAAAGTTG 11

RESULT 496
US-10-257-017B-187028/c
; Sequence 187028, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187028
; LENGTH: 13
```

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187028

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 497
US-10-257-017B-215785
; Sequence 215785, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 215785
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215785

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 11

RESULT 498
US-10-257-017B-215786/c
; Sequence 215786, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 215786
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215786

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 11

RESULT 499
US-10-257-017B-235787/c
; Sequence 235788, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235787
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235787

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 11

RESULT 500
US-10-257-017B-235788/c
; Sequence 235788, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235788
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235788

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3
```

```

Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 499
US-10-257-017B-235787
; Sequence 235787, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235787
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235787

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 11

RESULT 500
US-10-257-017B-235788/c
; Sequence 235788, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235788
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235788

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3
```

Search completed: December 3, 2007, 22:10:54
Job time : 17732 secs

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RESULT 1
PCT-US07-11121-41/c
; Sequence 41, Application PC/TUS0711121
; GENERAL INFORMATION:
; APPLICANT: Hitachi Chemical Co., Ltd.
; APPLICANT: Hitachi Chemical Research Center, Inc.
; APPLICANT: Hitachi Chemical Research Center, Inc.
; APPLICANT: Mitsuhashi, Masato
; APPLICANT: Ibara, Kazuhiko
; TITLE OF INVENTION: Method for Testing Drug Sensitivity in
; Solid Tumor Invention: Solid Tumors by Quantifying mRNA Expression in Thinly-Sliced
; Tumor Tissue
; FILE REFERENCE: HITACHI.081VPC
; CURRENT APPLICATION NUMBER: PCT/US07/11121
; CURRENT FILING DATE: 2007-09-19
; PRIOR APPLICATION NUMBER: PCT/US2007/011121
; PRIOR FILING DATE: 2007-05-08
; PRIOR APPLICATION NUMBER: US 60/798,674
; PRIOR FILING DATE: 2006-05-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Fast-Seq for Windows Version 4.0

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c 227	8.4	70.0	42.0	12	10	US-10-257-017B-312793	Sequence 3
c 228	8.4	70.0	42.0	12	10	US-10-257-017B-316105	Sequence 3
c 229	8.4	70.0	42.0	12	10	US-10-257-017B-316407	Sequence 3
c 230	8.4	70.0	42.0	12	10	US-10-257-017B-316596	Sequence 3
c 231	8.4	70.0	42.0	12	10	US-10-257-017B-317245	Sequence 3
c 232	8.4	70.0	42.0	12	10	US-10-257-017B-317868	Sequence 3
c 233	8.4	70.0	42.0	12	10	US-10-257-017B-317906	Sequence 3
c 234	8.4	70.0	42.0	12	10	US-10-257-017B-318475	Sequence 3
c 235	8.4	70.0	42.0	12	10	US-10-257-017B-321495	Sequence 3
c 236	8.4	70.0	42.0	12	10	US-10-257-017B-322078	Sequence 3
c 237	8.4	70.0	42.0	12	10	US-10-257-017B-323774	Sequence 3
c 238	8.4	70.0	42.0	12	10	US-10-257-017B-323855	Sequence 3
c 239	8.4	70.0	42.0	12	10	US-10-257-017B-327363	Sequence 3
c 240	8.4	70.0	42.0	12	10	US-10-257-017B-328966	Sequence 3
c 241	8.4	70.0	42.0	12	10	US-10-257-017B-329138	Sequence 3
c 242	8.4	70.0	42.0	12	10	US-10-257-017B-329589	Sequence 3
c 243	8.4	70.0	42.0	12	10	US-10-257-017B-329753	Sequence 3
c 244	8.4	70.0	42.0	12	10	US-10-257-017B-331303	Sequence 3
c 245	8.4	70.0	42.0	12	10	US-10-257-017B-331432	Sequence 3
c 246	8.4	70.0	42.0	12	10	US-10-257-017B-331579	Sequence 3
c 247	8.4	70.0	42.0	12	10	US-10-257-017B-331707	Sequence 3
c 248	8.4	70.0	42.0	12	10	US-10-257-017B-332215	Sequence 3
c 249	8.4	70.0	42.0	12	10	US-10-257-017B-332855	Sequence 3
c 250	8.4	70.0	42.0	12	10	US-10-257-017B-333880	Sequence 3
c 251	8.4	70.0	42.0	12	10	US-10-257-017B-336184	Sequence 3
c 252	8.4	70.0	42.0	12	10	US-10-257-017B-336774	Sequence 3
c 253	8.4	70.0	42.0	12	10	US-10-257-017B-338774	Sequence 3
c 254	8.4	70.0	42.0	12	10	US-10-257-017B-338942	Sequence 3
c 255	8.4	70.0	42.0	12	10	US-10-257-017B-339290	Sequence 3
c 256	8.4	70.0	42.0	12	10	US-10-257-017B-341683	Sequence 3
c 257	8.4	70.0	42.0	12	10	US-10-257-017B-341694	Sequence 3
c 258	8.4	70.0	42.0	12	10	US-10-257-017B-341790	Sequence 3
c 259	8.4	70.0	42.0	12	10	US-10-257-017B-343124	Sequence 3
c 260	8.4	70.0	42.0	12	10	US-10-257-017B-343306	Sequence 3
c 261	8.4	70.0	42.0	12	10	US-10-257-017B-344303	Sequence 3
c 262	8.4	70.0	42.0	12	10	US-10-257-017B-346809	Sequence 3
c 263	8.4	70.0	42.0	12	10	US-10-257-017B-347105	Sequence 3
c 264	8.4	70.0	42.0	12	10	US-10-257-017B-347310	Sequence 3
c 265	8.4	70.0	42.0	12	10	US-10-257-017B-347597	Sequence 3
c 266	8.4	70.0	42.0	12	10	US-10-257-017B-348478	Sequence 3
c 267	8.4	70.0	42.0	12	10	US-10-257-017B-352722	Sequence 3
c 268	8.4	70.0	42.0	12	10	US-10-257-017B-352762	Sequence 3
c 269	8.4	70.0	42.0	12	10	US-10-257-017B-352880	Sequence 3
c 270	8.4	70.0	42.0	12	10	US-10-257-017B-353886	Sequence 3
c 271	8.4	70.0	42.0	12	10	US-10-257-017B-354932	Sequence 3
c 272	8.4	70.0	42.0	12	10	US-10-257-017B-355010	Sequence 3
c 273	8.4	70.0	42.0	12	10	US-10-257-017B-358202	Sequence 3
c 274	8.4	70.0	42.0	12	10	US-10-257-017B-359017	Sequence 3
c 275	8.4	70.0	42.0	12	10	US-10-257-017B-359643	Sequence 3
c 276	8.4	70.0	42.0	12	10	US-10-257-017B-361463	Sequence 3
c 277	8.4	70.0	42.0	12	10	US-10-257-017B-361738	Sequence 3
c 278	8.4	70.0	42.0	12	10	US-10-257-017B-361979	Sequence 3
c 279	8.4	70.0	42.0	12	10	US-10-257-017B-362769	Sequence 3
c 280	8.4	70.0	42.0	12	10	US-10-257-017B-363267	Sequence 3
c 281	8.4	70.0	42.0	12	10	US-10-257-017B-363675	Sequence 3
c 282	8.4	70.0	42.0	12	10	US-10-257-017B-364075	Sequence 3
c 283	8.4	70.0	42.0	12	10	US-10-257-017B-364597	Sequence 3
c 284	8.4	70.0	42.0	12	10	US-10-257-017B-366105	Sequence 3
c 285	8.4	70.0	42.0	12	10	US-10-257-017B-366773	Sequence 3
c 286	8.4	70.0	42.0	12	10	US-10-257-017B-366978	Sequence 3
c 287	8.4	70.0	42.0	12	10	US-10-257-017B-367247	Sequence 3
c 288	8.4	70.0	42.0	12	10	US-10-257-017B-367323	Sequence 3
c 289	8.4	70.0	42.0	12	10	US-10-257-017B-367903	Sequence 3
c 290	8.4	70.0	42.0	12	10	US-10-257-017B-369031	Sequence 3
c 291	8.4	70.0	42.0	12	10	US-10-257-017B-369870	Sequence 3
c 292	8.4	70.0	42.0	12	10	US-10-257-017B-371139	Sequence 3
c 293	8.4	70.0	42.0	12	10	US-10-257-017B-371396	Sequence 3
c 294	8.4	70.0	42.0	12	10	US-10-257-017B-371986	Sequence 3
c 295	8.4	70.0	42.0	12	10	US-10-257-017B-373586	Sequence 3
c 296	8.4	70.0	42.0	12	10	US-10-257-017B-374860	Sequence 3
c 297	8.4	70.0	42.0	12	10	US-10-257-017B-375464	Sequence 3
c 298	8.4	70.0	42.0	12	10		
c 299	8.4	70.0	42.0	12	10		

ALIGNMENTS

RESULT 1

US-09-908-147-64

; Sequence 64, Application US/09908147

; Publication No. US20030144221A1

; GENERAL INFORMATION:

; APPLICANT: Hong Zhang

; APPLICANT: Andrew T. Watt

; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION

; FILE REFERENCE: RTS-0185

; CURRENT APPLICATION NUMBER: US/09/908.147

; CURRENT FILING DATE: 2001-07-17

; NUMBER OF SEQ ID NOS: 168

; SEQ ID NO 64

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-908-147-64

Query Match 100.0%; Score 20; DB 3; Length 20;

Score over Length 100.0%;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAAGTTCGCGT 20

|||||

Db 1 GCCCAGTTGAAGTTCGCGT 20

|||||

RESULT 2

US-10-728-509-64

; Sequence 64, Application US/10728509

; Publication No. US20040077583A1

; GENERAL INFORMATION:

; APPLICANT: Hong Zhang

; APPLICANT: Andrew T. Watt

; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION

; FILE REFERENCE: RTS-0185

; CURRENT APPLICATION NUMBER: US/10/728.509

; CURRENT FILING DATE: 2003-12-05

; PRIOR APPLICATION NUMBER: US/09/908.147

; PRIOR FILING DATE: 2001-07-17

; NUMBER OF SEQ ID NOS: 168

; SEQ ID NO 64

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-10-728-509-64

Query Match 100.0%; Score 20; DB 9; Length 20;

Score over Length 100.0%;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAAGTTCGCGT 20

|||||

Db 1 GCCCCAGTTGAAGTTGCCG 20

RESULT 3

US-09-908-147-65
; Sequence 65, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-65

Query Match 90.0%; Score 18; DB 3; Length 20;
Score over Length 90.0%;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTTGCC 18
Db 3 GCCCCAGTTGAAGTTGCC 20

RESULT 4

US-10-728-509-65
; Sequence 65, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-65

Query Match 90.0%; Score 18; DB 9; Length 20;
Score over Length 90.0%;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTTGCC 18
Db 3 GCCCCAGTTGAAGTTGCC 20

RESULT 5

US-09-908-147-5
; Sequence 5, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION

; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-908-147-5

Query Match 75.0%; Score 15; DB 3; Length 18;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
Db 4 GCCCCAGTTGAAGTT 18

RESULT 6

US-10-728-509-5
; Sequence 5, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-728-509-5

Query Match 75.0%; Score 15; DB 9; Length 18;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
Db 4 GCCCCAGTTGAAGTT 18

RESULT 7

US-10-257-017B-271773/c
; Sequence 271773, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 271773
; LENGTH: 12
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002613
US-10-257-017B-271773

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 8
US-10-257-017B-274756/c
; Sequence 274756, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 274756
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003668
US-10-257-017B-274756

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 9
US-10-257-017B-310208
; Sequence 310208, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310208
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863
US-10-257-017B-310208
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```

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10

RESULT 10
US-10-257-017B-341473/c
; Sequence 341473, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341473
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042053
US-10-257-017B-341473

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 11 AGTTGAAGTT 2

RESULT 11
US-10-257-017B-353251
; Sequence 353251, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353251
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048401
US-10-257-017B-353251

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10
|||||
|

RESULT 12
US-10-257-017B-355811/c
; Sequence 355811, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355811
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049826
US-10-257-017B-355811

Query Match 50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAAGTT 1
|||||
|

RESULT 13
US-09-908-147-119
; Sequence 119, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-119

Query Match 82.0%; Score 16.4; DB 3; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCCGT 20
DB 1 CCCAGTTGAAGTTGCCAT 18
|||||
|

RESULT 14
US-10-728-509-119
; Sequence 119, Application US/10728509
; Publication No. US20040077583A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-119

Query Match 82.0%; Score 16.4; DB 9; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCCGT 20
DB 1 CCCAGTTGAAGTTGCCAT 18
|||||
|

RESULT 15
US-08-591-486B-33
; Sequence 33, Application US/08591486B
; Publication No. US20020037866A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg F
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Göttingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
; TITLE OF INVENTION: Treatment of Neoplasms
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-9350
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-33
Query Match          57.0%; Score 11.4; DB 2; Length 14;
Score over Length    81.4%;
Best Local Similarity 92.3%; Pred. No. 2.3e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
    |||||
Db 2 GTTGAAGTTGCTG 14

RESULT 16
US-10-984-919-857
; Sequence 857, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763U0
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 857
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-857
Query Match          57.0%; Score 11.4; DB 11; Length 14;
Score over Length    81.4%;
Best Local Similarity 92.3%; Pred. No. 2.3e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
    |||||
Db 2 GTTGAAGTTGCTG 14

RESULT 17
US-10-138-674-4126/c
; Sequence 4126, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4126
Query Match          60.0%; Score 12; DB 9; Length 15;
Score over Length    80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
    |||||
Db 15 CCCAGTTGAAGT 4

RESULT 18
US-10-287-949A-4126/c
; Sequence 4126, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4126
Query Match          60.0%; Score 12; DB 9; Length 15;
Score over Length    80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
    |||||
Db 15 CCCAGTTGAAGT 4

RESULT 19
US-10-951-303-4126/c
; Sequence 4126, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-4126

Query Match      60.0%; Score 12; DB 11; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 20
US-11-088-219-4126/c
; Sequence 4126, Application US/11088219
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: MCSwiggan, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Fact
; TITLE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBH800-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-4126

Query Match      60.0%; Score 12; DB 23; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 21
US-10-257-017B-187031
; Sequence 187031, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187031
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187031

Query Match      52.0%; Score 10.4; DB 10; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 7.4e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 1 AGTTGAAGTTGC 12

RESULT 22
US-10-257-017B-187032/c
; Sequence 187032, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187032
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187032

Query Match      52.0%; Score 10.4; DB 10; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 7.4e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 13 AGTTGAAGTTGC 2

RESULT 23
US-11-495-951A-94101
; Sequence 94101, Application US/11495951A
; Publication No. US20070111227A1
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
```


; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94101
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-94101

Query Match 67.0%; Score 13.4; DB 27; Length 17;
Score over Length 78.8%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTCCGT 20
|||||
Db 3 AGTTGAAGTCCGT 17
|||||

RESULT 24
US-10-257-017B-275133/c
; Sequence 275133, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 275133
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003795
US-10-257-017B-275133

Query Match 47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 12 AGTTGAAGTTG 2
|||||

RESULT 25
US-10-257-017B-280261
; Sequence 280261, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280261
; LENGTH: 12
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008409
US-10-257-017B-280261

Query Match 47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 1 AGTTGAAGTTG 11
|||||

RESULT 26
US-10-257-017B-281972/c
; Sequence 281972, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010216
US-10-257-017B-281972

Query Match 47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
|||||
Db 11 AGTTGAGTTG 1
|||||

RESULT 27
US-10-257-017B-282569/c
; Sequence 282569, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 282569
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010870
US-10-257-017B-282569

```
Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      12 AGTTGAGTTG 2

RESULT 28
US-10-257-017B-300630
; Sequence 300630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300630
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019120
US-10-257-017B-300630

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      2 AGTTGAGTTG 12

RESULT 29
US-10-257-017B-305246
; Sequence 305246, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305246
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021354
US-10-257-017B-305246

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 AGTTGAAGTTG 16
DB      2 AGTTGAGTTG 12

RESULT 30
US-10-257-017B-314348
; Sequence 314348, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314348
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026294
US-10-257-017B-314348

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      2 AGTTAAAGTTG 12

RESULT 31
US-10-257-017B-329434
; Sequence 329434, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329434
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034943
US-10-257-017B-329434

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      1 AGTAGAAGTTG 11
```

```
RESULT 32
US-10-257-017B-337757
; Sequence 337757, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337757
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004732
US-10-257-017B-337757

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTAGAAGTTG 11

RESULT 33
US-10-257-017B-339358/c
; Sequence 339358, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 339358
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040958
US-10-257-017B-339358

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AATTGAAGTTG 11

RESULT 34
US-10-257-017B-345090/c
; Sequence 345090, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 345090
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043868
US-10-257-017B-345090

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAAGTTG 11

RESULT 35
US-10-257-017B-361423
; Sequence 361423, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 361423
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052630
US-10-257-017B-361423

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAAGTTG 11

RESULT 36
US-10-257-017B-28743
; Sequence 28743, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 28743
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004732
US-10-257-017B-28743

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AATTGAAGTTG 11
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 28743
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356
US-10-257-017B-28743

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
        |||||
Db      1 AGTTGAAGTT 10

RESULT 37
US-10-257-017B-28744/c
; Sequence 28744, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 28744
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356
US-10-257-017B-28744

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
        |||||
Db      13 AGTTGAAGTT 4

RESULT 38
US-10-257-017B-65609
; Sequence 65609, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 65609
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271
US-10-257-017B-65609

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
        |||||
Db      4 AGTTGAAGTT 13

RESULT 39
US-10-257-017B-65610/c
; Sequence 65610, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 65610
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271
US-10-257-017B-65610

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
        |||||
Db      10 AGTTGAAGTT 1

RESULT 40
US-10-257-017B-107775
; Sequence 107775, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107775
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982
US-10-257-017B-107775

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 3 AGTTGAAGTT 12

RESULT 41
US-10-257-017B-107776/c
; Sequence 107776, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107776
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982
US-10-257-017B-107776

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGTT 2

RESULT 42
US-10-257-017B-131257
; Sequence 131257, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131257
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131257

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGTT 2
```

```
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 1 GTTGAAGTTG 10

RESULT 43
US-10-257-017B-131258/c
; Sequence 131258, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131258
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131258

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 13 GTTGAAGTTG 4

RESULT 44
US-10-257-017B-150111
; Sequence 150111, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150111
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150111

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
```

```
Db          |||||
            4 AGTTGAAGTT 13

RESULT 45
US-10-257-017B-150112/c
; Sequence 150112, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150112
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150112

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
        |||||
Db      10 AGTTGAAGTT 1

RESULT 46
US-10-257-017B-153411
; Sequence 153411, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 153411
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780
US-10-257-017B-153411

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
        |||||
Db      2 AGTTGAAGTGY 13

RESULT 47
US-10-257-017B-153412/c
; Sequence 153412, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 153412
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780
US-10-257-017B-153412

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
        |||||
Db      12 AGTTGAAGTGY 1

RESULT 48
US-10-257-017B-171651
; Sequence 171651, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171651
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787
US-10-257-017B-171651

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
        |||||
Db      2 AGTTGAAGTT 11

RESULT 49
US-10-257-017B-171652/c
; Sequence 171652, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

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; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171652
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787
US-10-257-017B-171652

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
        |||||
Db      12 AGTTGAAGTT 3

RESULT 50
US-11-051-720-809
; Sequence 809, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 809
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-051-720-809

Query Match      50.0%; Score 10; DB 21; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
        |||||
Db      3 GTTGAAGTTG 12

RESULT 51
US-11-043-842-704
; Sequence 704, Application US/11043842
; Publication No. US20060183131A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 1847.1004
; CURRENT APPLICATION NUMBER: US/11/043,842
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1028
; SEQ ID NO 704
; LENGTH: 13
; TYPE: DNA
```

```
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-043-842-704

Query Match      50.0%; Score 10; DB 22; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
        |||||
Db      3 GTTGAAGTTG 12

RESULT 52
US-10-535-164-454911/c
; Sequence 454911, Application US/10535164
; Publication No. US20070134655A1
; GENERAL INFORMATION:
; APPLICANT: BENTWICH, ITZHAK
; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and thereof
; FILE REFERENCE: 050992.0200.PCUS13
; CURRENT APPLICATION NUMBER: US/10/535,164
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 548156
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 454911
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Human
; OTHER INFORMATION:
US-10-535-164-454911

Query Match      64.0%; Score 12.8; DB 17; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 4.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CCCAGTTGAAGTTGCC 18
        |||||
Db      16 CCCAGGTGAAGTTGCC 1

RESULT 53
US-11-495-951A-101428/c
; Sequence 101428, Application US/11495951A
; Publication No. US2007011227A1
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101428
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-101428

Query Match      64.0%; Score 12.8; DB 27; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 4.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 CCCAGTTGAAGTTGC 17
||||| |||||||
Db 16 CCCAGGGAAGTTGC 1

RESULT 54

US-10-257-017B-272526
; Sequence 272526, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 272526
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonukleotid-Primer
US-10-257-017B-272526

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
|||||
Db 4 AGTTGAAGT 12

RESULT 55

US-10-257-017B-281370/c
; Sequence 281370, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281370
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009690
US-10-257-017B-281370

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15
|||||
Db 11 GTTGAAGTT 3

RESULT 56

US-10-257-017B-284630/c
; Sequence 284630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284630
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011911
US-10-257-017B-284630

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
|||||
Db 12 AGTTGAAGT 4

RESULT 57

US-10-257-017B-288152
; Sequence 288152, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 288152
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013396
US-10-257-017B-288152

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
|||||
Db 2 TTGAAGTTG 10

RESULT 58

US-10-257-017B-298602
; Sequence 298602, Application US/10257017B
; Publication No. US20040241651A1


```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298602
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018187
US-10-257-017B-298602

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGAAGTTGC 17
Db 4 TGAAGTTGC 12

RESULT 59
US-10-257-017B-298745
; Sequence 298745, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298745
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-Primer
US-10-257-017B-298745

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 60
US-10-257-017B-299931
; Sequence 299931, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299931
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018813
US-10-257-017B-299931

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10

RESULT 61
US-10-257-017B-303341/c
; Sequence 303341, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303341
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020445
US-10-257-017B-303341

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 11 AGTTGAAGT 3

RESULT 62
US-10-257-017B-305026
; Sequence 305026, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305026
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021217
US-10-257-017B-305026

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15
| | | | | | | |
Db 4 GTTGAAGTT 12

RESULT 63
US-10-257-017B-307994
; Sequence 307994, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307994
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022828
US-10-257-017B-307994

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15
| | | | | | | |
Db 4 GTTGAAGTT 12

RESULT 64
US-10-257-017B-310012
; Sequence 310012, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310012
; LENGTH: 12
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023776
US-10-257-017B-310012

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
| | | | | | | |
Db 2 TTGAAGTTG 10

RESULT 65
US-10-257-017B-319646/c
; Sequence 319646, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 319646
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029341
US-10-257-017B-319646

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
| | | | | | | |
Db 12 TTGAAGTTG 4

RESULT 66
US-10-257-017B-332564/c
; Sequence 332564, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 332564
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036994
US-10-257-017B-332564

```
Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 12 TTGAAGTTG 4

RESULT 67
US-10-257-017B-333972
; Sequence 333972, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 333972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037861
US-10-257-017B-333972

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 2 TTGAAGTTG 10

RESULT 68
US-10-257-017B-337673
; Sequence 337673, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337673
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039994
US-10-257-017B-337673

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 TTGAAGTTG 16
DB 2 TTGAAGTTG 10

RESULT 69
US-10-257-017B-338530/c
; Sequence 338530, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338530
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005251
US-10-257-017B-338530

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 12 TTGAAGTTG 4

RESULT 70
US-10-257-017B-338626/c
; Sequence 338626, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338626
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040587
US-10-257-017B-338626

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15
DB 9 GTTGAAGTT 1
```

```
RESULT 71
US-10-257-017B-342781
; Sequence 342781, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 342781
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042707
US-10-257-017B-342781

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 1 TTGAAGTTG 9

RESULT 72
US-10-257-017B-343923/c
; Sequence 343923, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343923
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043299
US-10-257-017B-343923

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 10 GTTGAAGTT 2

RESULT 73
US-10-257-017B-345821/c
; Sequence 345821, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 345821
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044228
US-10-257-017B-345821

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 9 GTTGAAGTT 1

RESULT 74
US-10-257-017B-358109
; Sequence 358109, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358109
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050957
US-10-257-017B-358109

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 1 TTGAAGTTG 9

RESULT 75
US-10-257-017B-360215/c
; Sequence 360215, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 360215
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050957
US-10-257-017B-360215/c
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 360215
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051979
US-10-257-017B-360215

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGT 14
DB      10 AGTTGAAGT 2

RESULT 76
US-10-257-017B-365894/c
; Sequence 365894, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 365894
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055428
US-10-257-017B-365894

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTG 16
DB      12 TTGAAGTTG 4

RESULT 77
US-10-257-017B-369254
; Sequence 369254, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369254
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057554
US-10-257-017B-369254

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTT 15
DB      4 GTTGAAGTT 12

RESULT 78
US-10-257-017B-369635/c
; Sequence 369635, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369635
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057764
US-10-257-017B-369635

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTG 16
DB      9 TTGAAGTTG 1

RESULT 79
US-10-257-017B-379943
; Sequence 379943, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379943
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063547
US-10-257-017B-379943

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
DB 4 AGTTGAAGT 12

RESULT 80

US-09-168-791-14/c

Sequence 14, Application US/09168791

Publication No. US20030100519A1

GENERAL INFORMATION:

APPLICANT: Richelson, Elliott

APPLICANT: Tyler, Beth Marie

APPLICANT: Cusack, Bernadette Marie

APPLICANT: Douglas, Christopher Lee

APPLICANT: Jansen, Karen

TITLE OF INVENTION: USING POLYAMIDE NUCLEIC ACID OLIGOMERS

TITLE OF INVENTION: TO ENGINEER A BIOLOGICAL RESPONSE

FILE REFERENCE: 07039/126001

CURRENT APPLICATION NUMBER: US/09/168,791

CURRENT FILING DATE: 1998-10-08

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 14

TYPE: DNA

ORGANISM: Rat

US-09-168-791-14

Query Match 52.0%; Score 10.4; DB 3; Length 14;
Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 7.4e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
DB 14 CAGATGAAGTTG 3

RESULT 81

US-10-799-238-14/c

Sequence 14, Application US/10799238

Publication No. US2004022489A1

GENERAL INFORMATION:

APPLICANT: Richelson, Elliott

APPLICANT: Tyler, Beth Marie

APPLICANT: Cusack, Bernadette Marie

APPLICANT: Douglas, Christopher Lee

APPLICANT: Jansen, Karen

TITLE OF INVENTION: USING POLYAMIDE NUCLEIC ACID OLIGOMERS

TITLE OF INVENTION: TO ENGINEER A BIOLOGICAL RESPONSE

FILE REFERENCE: 07039/126001

CURRENT APPLICATION NUMBER: US/10/799,238

CURRENT FILING DATE: 2004-03-12

PRIOR APPLICATION NUMBER: US/09/168,791

PRIOR FILING DATE: 1998-10-08

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 14

TYPE: DNA

ORGANISM: Rat

US-10-799-238-14

Query Match 52.0%; Score 10.4; DB 10; Length 14;

Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 7.4e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
DB 14 CAGATGAAGTTG 3

RESULT 82

US-10-257-017B-61663

Sequence 61663, Application US/10257017B

Publication No. US20040241651A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 61663

LENGTH: 13

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401

US-10-257-017B-61663

Query Match 48.0%; Score 9.6; DB 10; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17
DB 4 TTGAAGTTGY 13

RESULT 83

US-10-257-017B-61664/c

Sequence 61664, Application US/10257017B

Publication No. US20040241651A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 61664

LENGTH: 13

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401

US-10-257-017B-61664

Query Match 48.0%; Score 9.6; DB 10; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17

```
Db      10 TTGAAGTTGY 1
|||||
RESULT 84
US-10-138-674-5807
; Sequence 5807, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5807

Query Match      59.0%; Score 11.8; DB 9; Length 16;
Score over Length      73.8%;
Best Local Similarity  66.7%; Pred. No. 1.4e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGAAGTT 15
        |||||:||||:
Db      2 GACCCAGAUGAAGUU 16

RESULT 85
US-10-287-949A-5807
; Sequence 5807, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5807

Query Match      59.0%; Score 11.8; DB 9; Length 16;
Score over Length      73.8%;
Best Local Similarity  66.7%; Pred. No. 1.4e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGAAGTT 15
        |||||:||||:
Db      2 GACCCAGAUGAAGUU 16

RESULT 86
US-11-088-219-5807
; Sequence 5807, Application US/11088219
```

```
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Facto
; TITLE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBHB00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-5807

Query Match      59.0%; Score 11.8; DB 23; Length 16;
Score over Length      73.8%;
Best Local Similarity  66.7%; Pred. No. 1.4e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGAAGTT 15
        |||||:||||:
Db      2 GACCCAGAUGAAGUU 16

RESULT 87
US-10-714-333A-764639/c
; Sequence 764639, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-764639

Query Match      70.0%; Score 14; DB 15; Length 19;
Score over Length      73.7%;
Best Local Similarity  100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 88
US-11-083-784-764639/c
; Sequence 764639, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-764639

Query Match 70.0%; Score 14; DB 19; Length 19;
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 89
US-11-101-244-764639/c
; Sequence 764639, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-764639

Query Match 70.0%; Score 14; DB 20; Length 19;
```

```
Score over Length 73.7%;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 90
US-09-504-231A-1284/c
; Sequence 1284, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1284

Query Match 55.0%; Score 11; DB 3; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 91
US-09-274-553D-1284/c
; Sequence 1284, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
```


; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-4150

Query Match 55.0%; Score 11; DB 23; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
|||||
DB 15 CCAGTTGAAGT 5

RESULT 96

US-10-477-086-15
; Sequence 15, Application US/10477086
; Publication No. US2004023497A1
; GENERAL INFORMATION:
; APPLICANT: GONG, Da-Wei
; APPLICANT: SCHULDINER, Alan
; APPLICANT: YANG, Rongze

; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: UMB-01-032
; CURRENT APPLICATION NUMBER: US/10/477,086
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: PCT/US02/15103
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALT2 Exon 3, intron/exon junction, 3' splice acceptor
US-10-477-086-15

Query Match 44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13
|||||
DB 1 CCCAGTTGAAGT 12

RESULT 97

US-10-257-017B-275104/c
; Sequence 275104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8

; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 275104
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003785
US-10-257-017B-275104

Query Match 44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12
|||||
DB 12 GCCCCACTTTAA 1

RESULT 98

US-10-257-017B-290891
; Sequence 290891, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290891
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014559
US-10-257-017B-290891

Query Match 44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
|||||
DB 1 AGTTGATGTAGC 12

RESULT 99

US-10-257-017B-317181/c
; Sequence 317181, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8

```
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 317181
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027856
US-10-257-017B-317181

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TTGAAGTTGCCG 19
Db      12 TTGAGTTGGCG 1

RESULT 100
US-10-257-017B-322885
/ Sequence 322885, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 322885
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031095
US-10-257-017B-322885

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
Db      1 AGTAGAAGTGC 12

RESULT 101
US-10-257-017B-323132/c
/ Sequence 323132, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 323132
/ LENGTH: 12
/ TYPE: DNA
```

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031232
US-10-257-017B-323132

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGAA 12
Db      12 GCGCGAGTTGAA 1

RESULT 102
US-10-257-017B-326883
/ Sequence 326883, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 326883
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033322
US-10-257-017B-326883

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TGAAGTTGCCGT 20
Db      1 TGAGGTTGTCGT 12

RESULT 103
US-10-257-017B-327149/c
/ Sequence 327149, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 327149
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033464
US-10-257-017B-327149
```

```
Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAAGTTGGGT 1

RESULT 104
US-10-257-017B-344782
; Sequence 344782, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344782
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043703
US-10-257-017B-344782

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAGATTGC 12

RESULT 105
US-10-257-017B-353467
; Sequence 353467, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353467
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048527
US-10-257-017B-353467

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 9 TGAAGTTGCCGT 20
Db 1 TGAAGTGGACGT 12

RESULT 106
US-10-257-017B-358049/C
; Sequence 358049, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358049
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050929
US-10-257-017B-358049

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAAGTTGGAGT 1

RESULT 107
US-10-257-017B-369872
; Sequence 369872, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369872
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057857
US-10-257-017B-369872

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAGATTTC 12
```

```
RESULT 108
US-10-257-017B-373811
; Sequence 373811, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 373811
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060333
US-10-257-017B-373811

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 1 AGTTGATTTGC 12

RESULT 109
US-10-591-442-27/c
; Sequence 27, Application US/10591442
; Publication No. US20070161001A1
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-27

Query Match      44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 110
US-10-591-442-29/c
; Sequence 29, Application US/10591442
; Publication No. US20070161001A1
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-29

Query Match      44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 111
US-10-591-442-45/c
; Sequence 45, Application US/10591442
; Publication No. US20070161001A1
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-45

Query Match      44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 112
US-11-126-421-15
; Sequence 15, Application US/11126421
; Publication No. US20050214883A1
; GENERAL INFORMATION:
; APPLICANT: GONG, Da-Wei
; APPLICANT: SCHULDINER, Alan
; APPLICANT: YANG, Rongze
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: UMB-01-032
; CURRENT APPLICATION NUMBER: US/11/126,421
; CURRENT FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: PCT/US02/15103
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 37
```

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALT2 Exon 3, intron/exon junction, 3' splice acceptor
US-11-126-4421-15

```

Query Match	44.0%	Score 8.8;	DB 18;	Length 12;
Score over Length	73.3%			
Best Local Similarity	83.3%	Pred. No. 4.8e+06;		
Matches 10;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 2 CCCAGTTGAAG 13
||| ||| ||| |||
pb 1 CCCAGGTGATG 12

RESULT 113

```

US-11-585-939A-7/c
; Sequence 7, Application US/11585939A
; Publication No. US20070138013A1
; GENERAL INFORMATION:
; APPLICANT: HAYASHI, Miho
; APPLICANT: MORI, Kazuyoshi
; APPLICANT: MAEDA, Mizuo
; TITLE OF INVENTION: DNA SEPARATION DEVICE, AND LIGAND DNA
; FILE REFERENCE: 2006-1856A
; CURRENT APPLICATION NUMBER: US/11/585,939A
; CURRENT FILING DATE: 2006-10-25
; PRIOR APPLICATION NUMBER: JP 2005-311933
; PRIOR FILING DATE: 2005-10-26
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-585-939A-7

```

Query Match	44.0%;	Score 8.8;	DB 27;	Length 12;
Score over Length	73.3%;			
Best Local Similarity	83.3%;	Pred. No. 4.8e+06;		
Matches 10;	Conservative	0; Mismatches 2;	Indels	

Qy 2 CCCAGTTGAAG 13
||| ||| |||
Db 12 CCCAGCCGAAG 1

```

RESULT 114
US-10-310-914A-801404/c
; Sequence 801404, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kivuzat
; TITLE OF INVENTION: Bioinformatically detected
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 02000.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 801404

```

```
; SEQ ID NO 001104
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-801404
```

Query Match 69.0%; Score 13.8; DB 12; Length 19;

```
Score over Length      72.6%;
Best Local Similarity  88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 CCCAGTTGAAGTTGCC 18
|||
Db 17 CCACATTGAAGTTGCC 1

RESULT 115

```

US-10-257-017B-6223
; Sequence 6223, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nu
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 6223
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for de
US-10-257-017B-6223

```

Query Match	47.0%;	Score 9.4;	DB 10;	Length 13;
Score over Length	72.3%;			
Best Local Similarity	90.9%;	Pred. No. 2.4e+06;		
Matches 10;	Conservative	0;	Mismatches 1;	Indels

QY 6 AGTTGAAGTTG 16
||| |||||
db 3 AGTAGAAGTTG 13

```

RESULT 116
US-10-257-017B-6224/c
; Sequence 6224, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nu
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 6224
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for de
US-10-257-017B-6224

```

```
Query Match          47.0%;      Score 9.4;  DB 10;  Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%;      Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps
```

QY 6 AGTTGAAGTTG 16

```
Db      11  ACTGAAGTTG 1
|||||
RESULT 117
US-10-257-017B-12629
; Sequence 12629, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12629
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12629
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  AGTTGAAGTTG 16
|||||
Db      2  AGTTGATGTTG 12
|||||
RESULT 118
US-10-257-017B-12630/c
; Sequence 12630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12630
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  AGTTGAAGTTG 16
|||||
Db      12 AGTTGATGTTG 2
|||||
RESULT 119
US-10-257-017B-12630/c
; Sequence 12630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25055
; Sequence 25055, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25055
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25055
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TGAAGTTGCCG 19
|||||
Db      3  TGAAGTTGCCG 13
|||||
RESULT 120
US-10-257-017B-25056/c
; Sequence 25056, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25056
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25056
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TGAAGTTGCCG 19
|||||
Db      11 TGAAGTTGCCG 1
|||||
RESULT 121
US-10-257-017B-25081
; Sequence 25081, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25081
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006096
US-10-257-017B-25081

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      2 AGTGGAAGTTG 12
      ||| ||||| |||

RESULT 122
US-10-257-017B-25082/c
; Sequence 25082, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25082
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006096
US-10-257-017B-25082

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      12 AGTGGAAGTTG 2
      ||| ||||| |||

RESULT 123
US-10-257-017B-27969
; Sequence 27969, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27969
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007879
US-10-257-017B-27969

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAAGTTG 11
      ||| ||||| |||

RESULT 124
US-10-257-017B-27970/c
; Sequence 27970, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27970
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007879
US-10-257-017B-27970

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3
      ||| ||||| |||

RESULT 125
US-10-257-017B-36537
; Sequence 36537, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```



```
; SEQ ID NO 36537
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36537

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 ATTGAAGTTG 11

RESULT 126
US-10-257-017B-36538/c
; Sequence 36538, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 36538
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36538

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 ATTGAAGTTG 3

RESULT 127
US-10-257-017B-56753
; Sequence 56753, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 56753
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56754

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAATTTG 3

RESULT 128
US-10-257-017B-56754/c
; Sequence 56754, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 56754
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56754

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAATTTG 3

RESULT 129
US-10-257-017B-96965
; Sequence 96965, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96965

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
```

```
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56753

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAATTTG 11

RESULT 128
US-10-257-017B-56754/c
; Sequence 56754, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 56754
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56754

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAATTTG 3

RESULT 129
US-10-257-017B-96965
; Sequence 96965, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96965

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
```

Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
|||||
Db 1 TGAAGTTGCCG 11

RESULT 130
US-10-257-017B-96966/c
; Sequence 96966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96966
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96966

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
|||||
Db 13 TGAAGTTGCCG 3

RESULT 131
US-10-257-017B-111321
; Sequence 111321, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111321
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111321

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||

Db 3 AGTTGTAAGTTG 13

RESULT 132
US-10-257-017B-111322/c
; Sequence 111322, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111322
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111322

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
Db 11 AGTTGTAAGTTG 1

RESULT 133
US-10-257-017B-117287
; Sequence 117287, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117287
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345
US-10-257-017B-117287

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
Db 3 AGTTGTAAGTTG 13

RESULT 134
US-10-257-017B-117288/c

```
; Sequence 117288, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117288
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345
US-10-257-017B-117288

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||||| |||||
Db      11 AGTTGAGTTG 1

RESULT 135
US-10-257-017B-117509
; Sequence 117509, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117509
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385
US-10-257-017B-117509

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||||| |||||
Db      3 AGTTGAATG 13

RESULT 136
US-10-257-017B-117510/c
; Sequence 117510, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117510
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385
US-10-257-017B-117510

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||||| |||||
Db      11 AGTTGAATG 1

RESULT 137
US-10-257-017B-187027
; Sequence 187027, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187027
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187027

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||||| |||||
Db      1 AGTTGAAGTGG 11

RESULT 138
US-10-257-017B-187028/c
; Sequence 187028, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187028
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187028

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 139
US-10-257-017B-215785
; Sequence 215785, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 215785
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215785

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 140
US-10-257-017B-215786/c
; Sequence 215786, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 215786
```

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215786

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 141
US-10-257-017B-235787
; Sequence 235787, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235787
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235787

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      1 AGTTGAAGTTG 11

RESULT 142
US-10-257-017B-235788/c
; Sequence 235788, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235788
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
```

US-10-257-017B-235788

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
DB 13 AGTGGAGTTG 3

RESULT 143

US-10-257-017B-248349
; Sequence 248349, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 248349
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060684
US-10-257-017B-248349

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
|||||
DB 1 AGTTGAGTTG 11

RESULT 144

US-10-257-017B-248350/c
; Sequence 248350, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 248350
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060684
US-10-257-017B-248350

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTG 16
|||||
DB 13 AGTTGAGTTG 3

RESULT 145

US-08-591-486B-34
; Sequence 34, Application US/08591486B
; Publication No. US20020037866A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg F
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Göttingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
; TITLE OF INVENTION: Treatment of Neoplasms
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-9350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; TOPOLOGY: unknown
; STRANDEDNESS: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-34

Query Match 50.0%; Score 10; DB 2; Length 14;
Score over Length 71.4%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
|||||
DB 5 GTTGAAGTTG 14

RESULT 146
US-10-984-919-858
; Sequence 858, Application US/10984919

```
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlengersien, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 858
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-858

Query Match 50.0%; Score 10; DB 11; Length 14;
Score over Length 71.4%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 5 GTTGAAGTTG 14

RESULT 147
US-10-310-914A-1258144/c
; Sequence 1258144, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1258144
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1258144

Query Match 64.0%; Score 12.8; DB 12; Length 18;
Score over Length 71.1%;
Best Local Similarity 87.5%; Pred. No. 4.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
DB 17 CAGTTGAAGTGCAGT 2

RESULT 148
US-10-160-358-26
; Sequence 26, Application US/10160358
; Publication No. US20030198969A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Blegiecki, Karyn
; APPLICANT: Cappola, Gina-Marie
```

```
; APPLICANT: Koshiy, Beena
; APPLICANT: Monroe, Glen
; TITLE OF INVENTION: HAPLOTYPES OF THE TACR2 GENE
; FILE REFERENCE: TACR2 MMH-0225US
; CURRENT APPLICATION NUMBER: US/10/160,358
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/47394
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/247,649
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-160-358-26

Query Match 53.0%; Score 10.6; DB 8; Length 15;
Score over Length 70.7%;
Best Local Similarity 90.9%; Pred. No. 5.9e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
DB 4 CCAGTTGAAGT 14

RESULT 149
US-10-138-674-1646/c
; Sequence 1646, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1646

Query Match 60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
DB 17 CCCAGTTGAAGT 6

RESULT 150
US-10-138-674-1647/c
; Sequence 1647, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
```

```
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1647

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 16 CCCAGTTGAAGT 5

RESULT 151
US-10-138-674-6253/c
; Sequence 6253, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6253
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6253

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 152
US-10-138-674-6254/c
; Sequence 6254, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6254
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6254

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 12 CCCAGTTGAAGT 1

RESULT 153
US-10-138-674-8571/c
; Sequence 8571, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8571

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 14 CCCAGTTGAAGT 3

RESULT 154
US-10-287-949A-1646/c
; Sequence 1646, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1646

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
| | | | | | | | | |
Db 17 CCCAGTTGAAGT 6

RESULT 155
US-10-287-949A-1647/c
; Sequence 1647, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 3.0
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1647

Query Match 60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
| | | | | | | | | |
Db 16 CCCAGTTGAAGT 5

RESULT 156
US-10-287-949A-6253/c
; Sequence 6253, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 3.0
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6253
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6253

Query Match 60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
| | | | | | | | | |
Db 15 CCCAGTTGAAGT 4

RESULT 157

US-10-287-949A-6254/c
; Sequence 6254, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6254
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6254

Query Match 60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
| | | | | | | | | |
Db 12 CCCAGTTGAAGT 1

RESULT 158

US-10-287-949A-8571/c
; Sequence 8571, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8571

Query Match 60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
| | | | | | | | | |
Db 14 CCCAGTTGAAGT 3

RESULT 159

US-10-712-633-3654/c
; Sequence 3654, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela

APPLICANT: Sandberg, Jennifer
APPLICANT: Gordon, Gilad
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
FILE REFERENCE: MBH02-325PCT (400/047)
CURRENT APPLICATION NUMBER: US/10/712,633
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 09/708,690
PRIOR FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: US 09/870,161
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/334,461
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/138,674
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 5989
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3654
LENGTH: 17
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-712-633-3654

Query Match 60.0%; Score 12; DB 10; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||||
DB 14 CCCAGTTGAAGT 3

RESULT 160
US-10-951-303-1646/c
Sequence 1646, Application US/10951303
Publication No. US20050227937A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-K (400/021)
CURRENT APPLICATION NUMBER: US/10/951,303
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/09/685,664
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1646
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-951-303-1646

Query Match 60.0%; Score 12; DB 11; Length 17;

Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||||
DB 17 CCCAGTTGAAGT 6

RESULT 161
US-10-951-303-1647/c
Sequence 1647, Application US/10951303
Publication No. US20050227937A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-K (400/021)
CURRENT APPLICATION NUMBER: US/10/951,303
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/09/685,664
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1647
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-951-303-1647

Query Match 60.0%; Score 12; DB 11; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
|||||
DB 16 CCCAGTTGAAGT 5

RESULT 162
US-11-088-219-1646/c
Sequence 1646, Application US/11088219
Publication No. US20070042029A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-Q (400/266)
CURRENT APPLICATION NUMBER: US/11/088,219
CURRENT FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: 10/138,674
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 09/870,161
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 09/708,690
PRIOR FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: 09/371,722
PRIOR FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-1646

Query Match 60.0%; Score 12; DB 23; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
| | | | | | | | | | | | | | | |
Db 17 CCCAGTTGAAGT 6

RESULT 163

US-11-088-219-1647/c
; Sequence 1647, Application US/11088219
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; FILE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBH00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-1647

Query Match 60.0%; Score 12; DB 23; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
| | | | | | | | | | | | | | | |
Db 16 CCCAGTTGAAGT 5

RESULT 164

US-11-088-219-6253/c
; Sequence 6253, Application US/11088219
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; FILE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBH00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6253
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-6253

Query Match 60.0%; Score 12; DB 23; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
| | | | | | | | | | | | | | | |
Db 15 CCCAGTTGAAGT 4

RESULT 165

US-11-088-219-6254/c
; Sequence 6254, Application US/11088219
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; FILE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBH00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6254
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-6254

```
Query Match      60.0%; Score 12; DB 23; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 12 CCCAGTTGAAGT 1

RESULT 166
US-11-088-219-8571/c
; Sequence 8571, Application US/11088219
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBHB00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-8571

Query Match      60.0%; Score 12; DB 23; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 14 CCCAGTTGAAGT 3

RESULT 167
US-10-310-914A-1191074/c
; Sequence 1191074, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1191074
; LENGTH: 19
; TYPE: RNA
```

```
; ORGANISM: Human
US-10-310-914A-1191074

Query Match      67.0%; Score 13.4; DB 12; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCC 18
   |||||
Db 17 CCAGTTGAAGTTGCC 3

RESULT 168
US-10-714-333A-726378/c
; Sequence 726378, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726378
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-726378

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 17 AGTTGAAGTTGCCGT 3

RESULT 169
US-10-714-333A-726385/c
; Sequence 726385, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726385
; LENGTH: 19
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-726385

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 18 AGTTGAAGTTGCCGT 4

RESULT 170
US-10-714-333A-1192689/c
; Sequence 1192689, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192689
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1192689

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 16 AGTTGAAGTTGCCGT 2

RESULT 171
US-10-714-333A-1192696/c
; Sequence 1192696, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192696

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1192696

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 18 AGTTGAAGTTGCCGT 4

RESULT 172
US-10-714-333A-1192704/c
; Sequence 1192704, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1192704

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 18 AGTTGAAGTTGCCGT 4

RESULT 173
US-11-083-784-726378/c
; Sequence 726378, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
```

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; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726378
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-726378

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCCT 3

RESULT 174
US-11-083-784-726385/c
; Sequence 726385, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726385
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-726385

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 18 AGTTGAAGTTGCCCT 4

RESULT 175
US-11-083-784-1192689/c
; Sequence 1192689, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192689
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1192689

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCGT 3

RESULT 177
US-11-083-784-1192704/c
; Sequence 1192704, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192696
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1192696

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCGT 3

RESULT 176
US-11-083-784-1192696/c
; Sequence 1192696, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192696
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1192696

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCGT 3

RESULT 178
US-11-083-784-1192689/c
; Sequence 1192689, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784

; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 1192704

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-083-784-1192704

Query Match 67.0%; Score 13.4; DB 19; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 18 AGTTGAAGTGCCGT 4

RESULT 178

US-11-101-244-726378/c

; Sequence 726378, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 726378

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-726378

Query Match 67.0%; Score 13.4; DB 20; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 17 AGTTGAAGTGCCCT 3

RESULT 179

US-11-101-244-726385/c

; Sequence 726385, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 726385

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-726385

Query Match 67.0%; Score 13.4; DB 20; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 18 AGTTGAAGTGCCCT 4

RESULT 180

US-11-101-244-1192689/c

; Sequence 1192689, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 1192689

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-1192689

Query Match 67.0%; Score 13.4; DB 20; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 16 AGTTGAAGTGCCGT 2

RESULT 181

US-11-101-244-1192696/c

; Sequence 1192696, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192696
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1192696

Query Match 67.0%; Score 13.4; DB 20; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTGGCGT 20
|||||
DB 17 AGTTGAAGTGGCGT 3

RESULT 182

US-11-101-244-1192704/c
; Sequence 1192704, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1192704

Query Match 67.0%; Score 13.4; DB 20; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTGGCGT 20
|||||
DB 18 AGTTGAAGTGGCGT 4

RESULT 183

US-10-535-164-474753
; Sequence 474753, Application US/10535164
; Publication No. US20070134655A1
; GENERAL INFORMATION:

; APPLICANT: BENTWICH, ITZHAK

; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and thereo
; FILE REFERENCE: 050992.0200.PCUS13
; CURRENT APPLICATION NUMBER: US/10/535,164
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 548156
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 474753
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Human
US-10-535-164-474753

Query Match 56.0%; Score 11.2; DB 17; Length 16;
Score over Length 70.0%;
Best Local Similarity 68.8%; Pred. No. 2.9e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTTG 16
|||||
DB 1 GUCCGAGUGGAGCUG 16

RESULT 184

US-10-078-958-50/c
; Sequence 50, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:

; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-078-958-50

Query Match 42.0%; Score 8.4; DB 7; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10
|||||
DB 12 GCCCCAGTAG 3

RESULT 185

US-10-078-958-59/c
; Sequence 59, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:

; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958

; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 59
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-078-958-59

Query Match 42.0%; Score 8.4; DB 7; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTG 10
| | | | | | | | | |
Db 12 GCCCCAGTAG 3

RESULT 186

US-10-257-017B-269582/c
; Sequence 269582, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269582
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001812
US-10-257-017B-269582

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
| | | | | | | | | |
Db 10 AGTTGAAGTT 1

RESULT 187

US-10-257-017B-269967/c
; Sequence 269967, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269967
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002305
US-10-257-017B-269967

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001948
US-10-257-017B-269967

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
| | | | | | | | | |
Db 11 AGTTGAAGAT 2

RESULT 188

US-10-257-017B-270364/c
; Sequence 270364, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 270364
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002104
US-10-257-017B-270364

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
| | | | | | | | | |
Db 10 AGTTGAATTT 1

RESULT 189

US-10-257-017B-270867/c
; Sequence 270867, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 270867
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002305
US-10-257-017B-270867


```
Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAATTT 1

RESULT 190
US-10-257-017B-272438
; Sequence 272438, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 272438
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002817
US-10-257-017B-272438

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 3 AGTTGAATTT 12

RESULT 191
US-10-257-017B-272556/c
; Sequence 272556, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 272556
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002858
US-10-257-017B-272556

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
DB 11 AGTTAAGTT 2

RESULT 192
US-10-257-017B-274200
; Sequence 274200, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 274200
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003474
US-10-257-017B-274200

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 3 GTTGAAGTAG 12

RESULT 193
US-10-257-017B-274757/c
; Sequence 274757, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 274757
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003668
US-10-257-017B-274757

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTCGAAGTT 1
```

```
RESULT 194
US-10-257-017B-280041/c
; Sequence 280041, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280041
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008088
US-10-257-017B-280041

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      10 AGTTGAAGTT 1

RESULT 195
US-10-257-017B-281065
; Sequence 281065, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281065
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009391
US-10-257-017B-281065

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
Db      2 GTAGAAGTTG 11

RESULT 196
US-10-257-017B-281930/c
; Sequence 281930, Application US/10257017B
; Publication No. US20040241651A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281930
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010165
US-10-257-017B-281930

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
Db      11 GTTGTAGTTG 2

RESULT 197
US-10-257-017B-284490
; Sequence 284490, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284490
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011855
US-10-257-017B-284490

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      2 AGTGAAGTT 11

RESULT 198
US-10-257-017B-285659
; Sequence 285659, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 285659
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012392
US-10-257-017B-285659

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      1 AGTTGAAGTT 10

RESULT 199
US-10-257-017B-286867/c
; Sequence 286867, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 286867
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012861
US-10-257-017B-286867

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAAGTT 3

RESULT 200
US-10-257-017B-288407/c
; Sequence 288407, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 288407
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013497
US-10-257-017B-288407

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      12 GTTAAAGTTG 3

RESULT 201
US-10-257-017B-290224/c
; Sequence 290224, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290224
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014248
US-10-257-017B-290224

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGTAGTT 1

RESULT 202
US-10-257-017B-292655/c
; Sequence 292655, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292655
; LENGTH: 12
; TYPE: DNA
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015296
US-10-257-017B-292655

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAAGTT 3

RESULT 203
US-10-257-017B-292658/c
; Sequence 292658, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292658
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015297
US-10-257-017B-292658

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      11 AGTTGAAGAT 2

RESULT 204
US-10-257-017B-292707/c
; Sequence 292707, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292707
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015313
US-10-257-017B-292707
```

```

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGAAGTT 1

RESULT 205
US-10-257-017B-293121/c
; Sequence 293121, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293121
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015507
US-10-257-017B-293121
```

```

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAAGTT 3

RESULT 206
US-10-257-017B-293477/c
; Sequence 293477, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293477
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015632
US-10-257-017B-293477
```

```

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 6 AGTTGAAGTT 15
|||||||
Db 11 AGTTGAAGCT 2

RESULT 207

US-10-257-017B-293667/c
; Sequence 293667, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293667
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015722
US-10-257-017B-293667

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||||
Db 11 AGTTGAAGTT 2

RESULT 208

US-10-257-017B-294586/c
; Sequence 294586, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 294586
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016192
US-10-257-017B-294586

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||||
Db 11 AGTTGAAGTT 2

RESULT 209

US-10-257-017B-295090
; Sequence 295090, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295090
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016430
US-10-257-017B-295090

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
|||||
Db 2 GTTGAAGTTG 11

RESULT 210

US-10-257-017B-295284
; Sequence 295284, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295284
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016521
US-10-257-017B-295284

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||||
Db 3 AGTTGAAGTT 12

RESULT 211

US-10-257-017B-296295/c
; Sequence 296295, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 296295
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017012
US-10-257-017B-296295

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
||| |||||
Db 12 AGTAGAAGTT 3

RESULT 212
US-10-257-017B-296487
Sequence 296487, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 296487
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017101
US-10-257-017B-296487

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
||| |||||
Db 3 AGTAGAAGTT 12

RESULT 213
US-10-257-017B-297323
Sequence 297323, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 297323
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017523
US-10-257-017B-297323

FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 297323
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017523
US-10-257-017B-297323

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
||| |||||
Db 2 AGTTGAGTT 11

RESULT 214
US-10-257-017B-298042
Sequence 298042, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 298042
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017887
US-10-257-017B-298042

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
||| |||||
Db 3 GTTGAAGTTG 12

RESULT 215
US-10-257-017B-299239
Sequence 299239, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 299239
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017887
US-10-257-017B-299239

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299239
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018492
US-10-257-017B-299239

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
DB 3 ATTTGAAGTT 12

RESULT 216

US-10-257-017B-300438
; Sequence 300438, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300438
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019035
US-10-257-017B-300438

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
| | | | | | | |
DB 3 GTTAAAGTTG 12

RESULT 217

US-10-257-017B-302312
; Sequence 302312, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302312
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019928
US-10-257-017B-302312

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
DB 2 AGTTGAAGTT 11

RESULT 218

US-10-257-017B-302603/c
; Sequence 302603, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302603
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020078
US-10-257-017B-302603

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
DB 10 AGTTTAAAGTT 1

RESULT 219

US-10-257-017B-302958
; Sequence 302958, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302958
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020249
US-10-257-017B-302958

Query Match 42.0%; Score 8.4; DB 10; Length 12;

```
Score over Length 70.0%; Pred. No. 7.8e+06; Mismatches 1; Indels 0; Gaps 0;
Best Local Similarity 90.0%;
Matches 9; Conservative 0;

Qy 7 GTTGAAGTTG 16
Db 2 GTTGAAGATG 11

RESULT 220
US-10-257-017B-304877
; Sequence 304877, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 304877
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021148
US-10-257-017B-304877

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11

RESULT 221
US-10-257-017B-306204/C
; Sequence 306204, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306204
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021865
US-10-257-017B-306204

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11

RESULT 222
US-10-257-017B-306498
; Sequence 306498, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306498
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022053
US-10-257-017B-306498

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11

RESULT 223
US-10-257-017B-306928
; Sequence 306928, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306928
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022250
US-10-257-017B-306928

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 3 AGTTGAAGTT 12

RESULT 224
```



```
US-10-257-017B-309177
; Sequence 309177, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 309177
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023399
US-10-257-017B-309177

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 3 AGTTGAAGCT 12

RESULT 225
US-10-257-017B-310209
; Sequence 310209, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310209
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863
US-10-257-017B-310209

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10

RESULT 226
US-10-257-017B-310210
; Sequence 310210, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310210
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863
US-10-257-017B-310210

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTCG 10

RESULT 227
US-10-257-017B-312793
; Sequence 312793, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 312793
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025301
US-10-257-017B-312793

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 2 GTTGAAGTTG 11

RESULT 228
US-10-257-017B-316105/C
; Sequence 316105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316105
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027285
US-10-257-017B-316105
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
Db 10 AGTTAAAGTT 1
```

RESULT 229

```
US-10-257-017B-316407
; Sequence 316407, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316407
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027431
US-10-257-017B-316407
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 GTTGAAGTTG 16
Db 1 GTTGAATTG 10
```

RESULT 230

```
US-10-257-017B-316595/c
; Sequence 316595, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 316595
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027519
US-10-257-017B-316595
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 GTTGAAGTTG 16
Db 11 GTTGAATTG 2
```

RESULT 231

```
US-10-257-017B-316596/c
; Sequence 316596, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316596
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027519
US-10-257-017B-316596
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 GTTGAAGTTG 16
Db 11 GTTGAATTG 2
```

RESULT 232

```
US-10-257-017B-317245/c
; Sequence 317245, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317245
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027885
US-10-257-017B-317245

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 12 AATTGAAGTT 3

RESULT 233

US-10-257-017B-317868/c
; Sequence 317868, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317868
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028311
US-10-257-017B-317868

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 11 ATTGAAGTT 2

RESULT 234

US-10-257-017B-317906/c
; Sequence 317906, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317906
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-Primer
US-10-257-017B-317906

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 12 AATTGAAGTT 3

RESULT 235

US-10-257-017B-318475/c
; Sequence 318475, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 318475
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028677
US-10-257-017B-318475

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 10 AATTGAAGTT 1

RESULT 236

US-10-257-017B-321495/c
; Sequence 321495, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 321495
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030284
US-10-257-017B-321495

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
| | | | | | | |

```
Db      12 GTTGAAGTGG 3

RESULT 237
US-10-257-017B-322078/c
; Sequence 322078, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322078
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030647
US-10-257-017B-322078

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGAGTT 1

RESULT 238
US-10-257-017B-323774/c
; Sequence 323774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323774
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031607
US-10-257-017B-323774

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 ATTTGAAGTT 3

RESULT 239
US-10-257-017B-323855/c
```

```
; Sequence 323855, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323855
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031647
US-10-257-017B-323855

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      12 GTTGAAGTTG 3

RESULT 240
US-10-257-017B-327363/c
; Sequence 327363, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 327363
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033594
US-10-257-017B-327363

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      11 AGTTTAAAGTT 2

RESULT 241
US-10-257-017B-328966/c
; Sequence 328966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 328966
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034675
US-10-257-017B-328966

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 11 GTTAAAGTTG 2

RESULT 242
US-10-257-017B-329138/c
; Sequence 329138, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329138
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034774
US-10-257-017B-329138

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 15
Db 10 AGTTGAATTT 1

RESULT 243
US-10-257-017B-329589
; Sequence 329589, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331303
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035126
US-10-257-017B-329589

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 3 GTTGAATTTG 12

RESULT 245
US-10-257-017B-331303/c
; Sequence 331303, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331303
```

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329589
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035020
US-10-257-017B-329589

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 15
Db 2 AGTTAAAGTT 11

RESULT 244
US-10-257-017B-329753
; Sequence 329753, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329753
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035126
US-10-257-017B-329753

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 3 GTTGAATTTG 12

RESULT 245
US-10-257-017B-331303/c
; Sequence 331303, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331303
```

```

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036110
US-10-257-017B-331303

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAGGTTG 3

RESULT 246
US-10-257-017B-331432/c
; Sequence 331432, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331432
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036202
US-10-257-017B-331432

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAGGTTG 3

RESULT 247
US-10-257-017B-331579/c
; Sequence 331579, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331579
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036328

```

US-10-257-017B-331579

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGATGTT 2

RESULT 248

US-10-257-017B-331707/c
; Sequence 331707, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331707
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-Primer
US-10-257-017B-331707

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGAGTT 2

RESULT 249

US-10-257-017B-332215/c
; Sequence 332215, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 332215
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036773
US-10-257-017B-332215

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 11 AGTTGAAGTT 2

RESULT 250

US-10-257-017B-333855/c
; Sequence 333855, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 333855
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037792
US-10-257-017B-333855

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 11 AGTTGAAGTT 2

RESULT 251

US-10-257-017B-333880
; Sequence 333880, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 333880
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037804
US-10-257-017B-333880

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 3 AGTTGAAGTT 12

RESULT 252

US-10-257-017B-336184/c
; Sequence 336184, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 336184
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039238
US-10-257-017B-336184

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
|||||
Db 12 GTTGAAGTTG 3

RESULT 253

US-10-257-017B-338774/c
; Sequence 338774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338774
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040669
US-10-257-017B-338774

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 10 AGTTGAAGTT 1

RESULT 254

US-10-257-017B-338942
; Sequence 338942, Application US/10257017B

Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 338942
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040756
US-10-257-017B-338942

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
|||||
Db 1 GTTGAAGTAG 10

RESULT 255
US-10-257-017B-339290
Sequence 339290, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 339290
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007278
US-10-257-017B-339290

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
Db 2 AGTTGAATTT 11

RESULT 256
US-10-257-017B-341683
Sequence 341683, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 341683
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042183
US-10-257-017B-341683

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
|||||
Db 2 GTTGAAGTTG 11

RESULT 257
US-10-257-017B-341694/c
Sequence 341694, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 341694
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042185
US-10-257-017B-341694

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
|||||
Db 10 GTTGAAGTTG 1

RESULT 258
US-10-257-017B-341790/c
Sequence 341790, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341790
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042229
US-10-257-017B-341790

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 12 GTTAAAGTTG 3

RESULT 259
US-10-257-017B-342185/c
; Sequence 342185, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 342185
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042419
US-10-257-017B-342185

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 11 AGTTAAAGTT 2

RESULT 260
US-10-257-017B-343124
; Sequence 343124, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343124
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043488
US-10-257-017B-344303

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042902
US-10-257-017B-343124

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 2 AGTTAAAGTT 11

RESULT 261
US-10-257-017B-343306
; Sequence 343306, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343306
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010454
US-10-257-017B-343306

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 3 GTTAAAGTTG 12

RESULT 262
US-10-257-017B-344303
; Sequence 344303, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344303
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043488
US-10-257-017B-344303

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 2 AGTTTAAAGTT 11

RESULT 263

US-10-257-017B-346809
; Sequence 346809, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 346809
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044779
US-10-257-017B-346809

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 2 AGTTGAAGAT 11

RESULT 264

US-10-257-017B-347105/c
; Sequence 347105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347105
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044912
US-10-257-017B-347105

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 11 AGTTAAAGTT 2

RESULT 265

US-10-257-017B-347106/c
; Sequence 347106, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347106
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044912
US-10-257-017B-347106

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 11 AGTTAAAGTT 2

RESULT 266

US-10-257-017B-347275
; Sequence 347275, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347275
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045008
US-10-257-017B-347275

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
| | | | | | | |
Db 2 AGTTAAAGTT 11

RESULT 267
US-10-257-017B-347597/c
; Sequence 347597, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347597
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045181
US-10-257-017B-347597

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
||| ||| |||
Db 11 GTTGAATTG 2

RESULT 268
US-10-257-017B-348478/c
; Sequence 348478, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 348478
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045610
US-10-257-017B-348478

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
||| ||| |||
Db 11 ATTGAAGTT 2

RESULT 269
US-10-257-017B-352722
; Sequence 352722, Application US/10257017B
; Publication No. US20040241651A1

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 352722
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048058
US-10-257-017B-352722

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
||| ||| |||
Db 2 GTTTAAGTTG 11

RESULT 270
US-10-257-017B-352762/c
; Sequence 352762, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 352762
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048084
US-10-257-017B-352762

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
||| ||| |||
Db 10 AGTTGAGTT 1

RESULT 271
US-10-257-017B-352880/c
; Sequence 352880, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

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; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 352880
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048150
US-10-257-017B-352880

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAGTT 3

RESULT 272
US-10-257-017B-353886/c
; Sequence 353886, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353886
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048785
US-10-257-017B-353886

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAAGAT 3

RESULT 273
US-10-257-017B-354932
; Sequence 354932, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355310
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049419
US-10-257-017B-355010

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      3 AATTGAAGTT 12

RESULT 275
US-10-257-017B-355310/c
; Sequence 355310, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355310
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049419
US-10-257-017B-355010

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      3 AATTGAAGTT 12

RESULT 275
US-10-257-017B-355310/c
; Sequence 355310, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355310
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049419
US-10-257-017B-355010
```

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; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 354932
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010418
US-10-257-017B-354932

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      1 GTTGAAGTTG 10

RESULT 274
US-10-257-017B-355010
; Sequence 355010, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355010
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049419
US-10-257-017B-355010

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      3 AATTGAAGTT 12

RESULT 275
US-10-257-017B-355310/c
; Sequence 355310, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355310
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049419
US-10-257-017B-355010
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049589
US-10-257-017B-355310

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
|||||
DB 11 GTTGAGTTG 2

RESULT 276

US-10-257-017B-358202
; Sequence 358202, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358202
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050991
US-10-257-017B-358202

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
DB 3 AGTTGAAGAT 12

RESULT 277

US-10-257-017B-359017/c
; Sequence 359017, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359017
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051425
US-10-257-017B-359017

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
DB 11 AGTTGAGTT 2

RESULT 278

US-10-257-017B-359643
; Sequence 359643, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359643
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051694
US-10-257-017B-359643

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
|||||
DB 1 AGTTGAGTT 10

RESULT 279

US-10-257-017B-361463
; Sequence 361463, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 361463
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052647
US-10-257-017B-361463

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 3 AGTTGAAGTT 12

RESULT 280

US-10-257-017B-361738/c
; Sequence 361738, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 361738
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052802
US-10-257-017B-361738

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGTT 2

RESULT 281

US-10-257-017B-361979/c
; Sequence 361979, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 361979
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052975
US-10-257-017B-361979

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 12 AGTTGAAGTT 3

RESULT 282

US-10-257-017B-362769/c
; Sequence 362769, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 362769
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053437
US-10-257-017B-362769

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGATGAAGTT 1

RESULT 283

US-10-257-017B-363267
; Sequence 363267, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 363267
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053740
US-10-257-017B-363267

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 2 AATTGAAGTT 11

RESULT 284

US-10-257-017B-363675
; Sequence 363675, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

```
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 363675
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053997
US-10-257-017B-363675

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 AAGTTGCCGT 20
Db 3 AAGTTGTCCT 12

RESULT 285
US-10-257-017B-364075
; Sequence 364075, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364075
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0054253
US-10-257-017B-364075

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 1 AGTTGAGTT 10

RESULT 286
US-10-257-017B-364597/c
; Sequence 364597, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364597
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0054603
US-10-257-017B-364597

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GATGAAGTTG 3

RESULT 287
US-10-257-017B-366105/c
; Sequence 366105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 366105
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010825
US-10-257-017B-366105

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTGAAGTT 2

RESULT 288
US-10-257-017B-366773/c
; Sequence 366773, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 366773
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055962
US-10-257-017B-366773

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 10 GTTGAAGTTG 1

RESULT 289
US-10-257-017B-366978/c
; Sequence 366978, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 366978
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056077
US-10-257-017B-366978

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAAGTTG 3

RESULT 290
US-10-257-017B-367247
; Sequence 367247, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 367247
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056243
US-10-257-017B-367247
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
Db 1 AGTTAAAGTT 10
```

RESULT 291

```
US-10-257-017B-367323/c
; Sequence 367323, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 367323
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009154
US-10-257-017B-367323
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
Db 10 AGTTAAAGTT 1
```

RESULT 292

```
US-10-257-017B-369030
; Sequence 369030, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369030
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057415
US-10-257-017B-369030
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
```



```
Score over Length 70.0%; Pred. No. 7.8e+06;
Best Local Similarity 90.0%; 0; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 7 GTTGAAGTTG 16
DB 2 GGTGAAGTTG 11

RESULT 293
US-10-257-017B-369031
; Sequence 369031, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369031
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057415
US-10-257-017B-369031

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 2 GGTGAAGTTG 11

RESULT 294
US-10-257-017B-369870
; Sequence 369870, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369870
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057857
US-10-257-017B-369870

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
```

```
DB 1 AGTTGAAGTT 10

RESULT 295
US-10-257-017B-371399
; Sequence 371399, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 371399
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058753
US-10-257-017B-371399

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10

RESULT 296
US-10-257-017B-371986
; Sequence 371986, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 371986
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0059100
US-10-257-017B-371986

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10

RESULT 297
```

```
US-10-257-017B-373586
; Sequence 373586, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 373586
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060183
US-10-257-017B-373586

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      1 AGTTGTAGTT 10

RESULT 298
US-10-257-017B-374860
; Sequence 374860, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 374860
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060940
US-10-257-017B-374860

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      2 GTTGAATTG 11

RESULT 299
US-10-257-017B-375464/c
; Sequence 375464, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 375464
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061264
US-10-257-017B-375464

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTGGAAGTT 1

RESULT 300
US-10-257-017B-375689
; Sequence 375689, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 375689
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0000447
US-10-257-017B-375689

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      2 ATTTCGAAGTT 11

RESULT 301
US-10-257-017B-375855/c
; Sequence 375855, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
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; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 375855
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061481
US-10-257-017B-375855

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      10 AGTTTAAAGTT 1

RESULT 302
US-10-257-017B-376089
; Sequence 376089, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376089
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061604
US-10-257-017B-376089

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
Db      1 GTGGAAGTTG 10

RESULT 303
US-10-257-017B-376898/c
; Sequence 376898, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
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; SEQ ID NO 376898
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062033
US-10-257-017B-376898

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      11 AGTTGAAGTT 2

RESULT 304
US-10-257-017B-377382/c
; Sequence 377382, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 377382
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062298
US-10-257-017B-377382

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      11 AATTGAAGTT 2

RESULT 305
US-10-257-017B-379629/c
; Sequence 379629, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379629
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063392
US-10-257-017B-379629

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
| | | | | | | |
Db 10 AGTTGAAGTT 1

RESULT 306
US-10-257-017B-380089
; Sequence 380089, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 380089
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063628
US-10-257-017B-380089

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
| | | | | | | |
Db 1 AGTTGAAGTT 10

RESULT 307
US-10-708-951-20463/c
; Sequence 20463, Application US/10708951
; Publication No. US20070042982A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20463
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-20463

Query Match 42.0%; Score 8.4; DB 16; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 12
| | | | | | | |

Db 12 CCCAGTTGTA 3

RESULT 308
US-10-708-951-46965/c
; Sequence 46965, Application US/10708951
; Publication No. US20070042982A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46965
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-46965

Query Match 42.0%; Score 8.4; DB 16; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 12
| | | | | | | |
Db 12 CCCAGTTGTA 3

Search completed: December 3, 2007, 18:13:57
Job time : 1307 secs